

## FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCG  
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG  
CTGTGCGCGCCGCGCCGGAGGCCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT  
GGTGGAACAAGTTTAACCAAGGGATGGTGGACACCGCAAAGAAGAACTTTGGCCGCGGGAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCGTGCTGGAGATC  
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGACTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA  
GGGCGACGGGTCTGCGCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCAGTGTGAAGTGGGCTGGGTGCT  
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCTGCGAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG  
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCGAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG  
AAAACTGCTACAATACTCCAGGGAGTACGTCTGTGTGTCTCTGACGGCTTCGAAGAAACG  
GAAGATGCCTGTGTGCCGCCGCGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT  
GCCCTCCCGCAAGACCTGTAATGTGCGGACTTACCCTTTAAATTATTCAGAAGGATGTCC  
CGTGAAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTTAAACAGCTGCATTTCTTGTTGTCTTTA  
AACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCCACTTGTTTATGTCAGCTTATAATGGTTACAATAAAGCAATAGCA  
TCACAAATTTACAAATAAAGCATTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACT  
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGCCGAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG  
TGTGTCAGTAGGGTGTGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRLVDKFNQGMVD TAKKNFGGGNTAWEKTL SKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKT LKVCSPGTYGPDCLACQGGSGRPCSG  
NGHCSDGSGRQGDGSCRMGYQGPLECTDCMDGYFSSLRNETHS ICTACDESKCTCSGLTNRCGCEVGVWLDE  
GACVDVDECAAEPPPCSAQAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA EKT  
CVRKNENCYNTPGSYVCVCPDGFEE TEDACVPPAEAEATEGESPTQLPSREDL

### **Signal peptide:**

amino acids 1-24

### **N-glycosylation sites.**

amino acids 190-194 and 251-255

### **Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

### **Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

### **Tyrosine kinase phosphorylation site.**

amino acids 303-310

### **N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

### **EGF-like domain cysteine pattern signature.**

amino acids 166-178

### **Leucine zipper pattern.**

amino acids 94-116

# FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCCGGGGATCCTCTAGAGATCCCTC  
 GACCTCGACCACCGCGTCCGCCAGGCCGGGAGGCGACGCCGCCAGCCGTCTAAACCGGGAACA  
 GCCTTGGCTGAGGGAGCTGCAGCCAGCAGAGTATCTGACGGCCCGAGGTTGCGTAGGTGCG  
 GCACGAGGAGTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGCCCGGAGGAGCGCCTTC  
 CCTGCCCGCGCGCTCTGGCTCTGGAGCATCTCTGTGCTGCTGGCACTGCGGGCGGAGGC  
 CGGGCCCGCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTACCAAGGCAAGAGTACTCA  
 TAGGATTGAAGAAGATATCTCTGATTGTTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT  
 TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC  
 CTGGCAAGCTGCAGGGCAGGCAGAACTACTTCTATGAATTCCTGTCTTTGCGCTCCCTGGATA  
 AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA  
 TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGAAAAACAGGATGGGGTGGCAGCATTTGAAGT  
 GGATGTGATTGTTATGAATCTGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCT  
 TCTTTAAACATGTCAACAGCTGAGTGCCCGAGGCGGGTGCCGAAATGGAGGCTTTTGTAAAT  
 GAAAGACGCATCTGCGAGTGCTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG  
 TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG  
 GATTCTATGGAGTGAACCTGTGACAAAGCAAACCTGCTCAACCACTGCTTTAATGGAGGACC  
 TGTTTCTACCTGGAAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
 CAAATGCCCCAACCCCTGTGCAAAATGGAGGTAAATGCATTTGGTAAAAAGCAAATGTAAGTGT  
 CCAAAGGTTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACAT  
 GGAACCTGCCATGAACCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
 TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC  
 ACACGCCTTCACTTAAAAAGGCCGAGGAGCGCGGGATCCACCTGAATCCAATTACATCTGG  
TGAACTCCGACATCTGAACCGTTTAAAGTTACACCAAGTTTATAGCCTTTGTAACTTTCA  
 TGTGTTGAATGTTCAAATAATGTTTATTACACTTAAGAATACTGGCTGAATTTTATTAGCT  
 TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTTAAAGTTTCTAAGTACGTCTGTAG  
 CATGATGGTATAGATTTTCTGTTTCAGTGCTTTGGGACAGATTTTATATATATGTCAATTGA  
 TCAGGTTAAATTTTTCAGTGTGTAGTTGGCAGATATTTCAAATAACAAATGATGATTTATGGT  
 GTCTGGGGGCGAGGGAACATCAGAAAGGTTAAATGGGCAAAAATGCGTAAGTCACAAGAAT  
 TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAGATTTTATTGTGATATTTAGAT  
 GTTTGTTACATTTTAAAAAATTGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACC  
 TTACCATTTATCCAGAGATTCAGTATTAACAAAAAATTAACACTGTGGTAGTGGCATTT  
 AAACAATATAATATATTTTAAACACAATGAATAGGGAATATAATGTATGAACCTTTTTCAT  
 TGGCTTGAAGCAATATAATATATTTGTAACAAAAACAGCTCTTACCTAATAAACATTTTAT  
 ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTGGGAAAAAAGGAAAAA  
 AAAAAAAGGAAAAAAGGCGCGCAGCTAGAGTGCACCTGCAGAGCTTGGC  
 CGCCATGGCCCAACTGTTTATTGTCAGCTTATAATG

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## FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094  
><subunit 1 of 1, 379 aa, 0 stop  
><MW: 41528, pI: 7.97, NX(S/T): 2  
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEEISLYLWIDAHQARVLIGFEEDILIVSEGK  
MAPPTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL  
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC  
RNGGFCNERRICECPDGFHGFHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST  
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPV  
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP  
PESNYIW

### **Signal peptide:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 88-92, 245-249

### **Casein kinase II phosphorylation site.**

amino acids 319-323

### **Tyrosine kinase phosphorylation site.**

amino acids 370-378

### **N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

### **ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

### **EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

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## FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGAGGCGCGGGGCCAGCCTGGG  
CCCCAGCCCCACCTTCACCAGGGCCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCTGGGCGCCGG  
GAGCTAGCACCCGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT  
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCTTTTCCCCGATCCAGGATGTATGATGGAGGTCGTATCTA  
TCCAGTCTTGGGAACGTACTGGGACAACCTGTAACCGTTGCACTGGCAGGAGAACAGGCAGT  
GGCATGTTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGCGCTTCTGGGGCATGACCTGGATGAGGGGCATTCGCTACCCGCTGGGACCA  
TCCGCCCATCTTCTCGGTATGAACATGCATGAAATTTATACAGTGTGAACCCAGGGGAG  
GTGCTTCCACAGCCTTCGAGGCCCTCTGAGAAGTGGCCAACTGATTATGAGCCTCTTGA  
CCAAGGCAACTGTGCAGGCTCTGGGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCGGGACACATGACGCTGTCTGTGCGCCAGAACCTGCTGTCTTGTGAC  
ACCCACAGCAGCAGGGCTGCCGCGTGGGCGTCTCGATGGTGCCTGGTGGTCTCTGCGTCTG  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGACAGCCGAGCCATGGGTGGGGCAAGCGCCAGGCCACTGCC  
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC  
CTTGGGAGGCCAGAGATACCGCGCATGGGACCCACTCAGTCAAGATCACAGGATGGG  
AGAGGAGACGTGCGAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCTGGGGCC  
CAGCCTGGGGCGAGAGGGGCCATTCGCGATCGTGCGCGGCTCAATGAGTGCGACATCGAG  
AGCTTCGTGCTGGGCGTCTGGGGCGCGTGGGCATGGAGACATGGGTCACTGAGGCTG  
CGGGCACCACGCGGGTCCGGCTGGGATCCAGGCTAAGGGCCGCGGGAAGAGGCCCAATG  
GGGCGGTGACCCAGCCTCGCCGACAGAGCCCGGGCGCAGGCGGGCGCCAGGGCGCTAAT  
CCCGCGCGGGTTCGCTGACGACGCGCCCGCCTGGGAGCCGCGGCGAGGCGAGACTGGCG  
GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCAGAGCTGCAG  
ATCCAGGCCTTGGGCGCCCACTCAAGACTACCAAAGCAGGACCTCAAGTCTCCAGC  
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTATAGACAGGCTTGTCTCCG  
TTGCCAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA  
AGTGACCTCCCACTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCAACCAACACCTGGC  
TAATTTTTGTATTTTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAACT  
CCTGGGCTCAAGCGGTCCACCTGCCTCGCCTCCCAAAGTGCTGAGGATGAGGC  
ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTCTTTTCACTGTTTTAAAA  
TAAACCAAAGTATTGATAAAAAAAA

0993925.071101

## **FIGURE 6**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223  
><subunit 1 of 1, 164 aa, 1 stop  
><MW: 18359, pI: 7.45, NX(S/T): 1  
MWRCPLGLLLLLPLAGHLALGAQQGGRRELAPGLHLRGIRDAGGRYCQEQDLCCRGRADD  
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYFVLGTYWDNCNR  
CTCQENRQWHGGSRRHDQSHQPGQLWLAGWEPQRLLGHDPG

### **N-glycosylation site.**

amino acids 78-82, 161-165

### **Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

### **N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

### **Amidation site.**

amino acids 26-30, 318-322

### **Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

[illegible]

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCMATCCCATTCTGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCTGTCTTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC  
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCTGGTGGTTCTCTGCGTGC CGCAGG  
GNTGGTGTCTGACCAC TGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTTCGGGGCAAGCGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGTGCACTCTCTGTCTACCGCCTCGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGTAGGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGGAGGACTTCTCTGTATACAAGGAGGAGGCATCTACGCCACACGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

## **FIGURE 8**

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACGTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTGGGAGCCTGTCCTGGTTCTTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCC GG CAGA  
TCAGTCTTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAAACCCTCTCTGTGCTGTTTC  
CATGGCC CAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCAGGAAGCCTT  
CCCTGCCCCCCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACC CAGCA  
GGGGACAGGCACTCAGGAGGGCCAGTAAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCCCTGGGAGTCTCCAGAGATGGGGCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAA



## **FIGURE 9**

MTHRTTTWARTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPDPPMALSRTPTRQISSDT  
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVNSVVS PAPS RGQAL RRAQ

### **Signal peptide:**

amino acids 1-47

### **N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

### **N-myristoylation site.**

amino acids 56-60

### **Amidation site.**

amino acids 70-74

## FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGGAGCCGCCCGCCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAAGTACACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC  
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG  
CGTGTTCACGGAGATCGTGCTGGAGAACAACTATACGGCCTTCCAGAACGCCCGGCACGAGG  
GCTGGTTCATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC  
CAGCGCGAGGCCCACCTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCAGC  
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGACCAAGCGCACAC  
GGCGGCCCCAGCCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCCGCTCCC  
CACCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGCTGGCGGAGGGGAGCCAGATCCC  
GAGGGAGGACCCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGCTG  
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAAC  
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC  
CGCTGAAAGGTGAGCGACTGAAGGCCTTGCAAGACAACCGTCTGGAGGTGGCTGTCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCAACTCCTCCTGGCTAGACTGTA  
GGAAGGCACTTTTGTTTGTTTGTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAAATAG  
AGGGTTGTCCACTCCTCACATTCACGACCCAGGCCTGCACCCACCCCCAACTCCAGCCC  
CGGAATAAAACCATTTTCTGC

090322.07104

## **FIGURE 11**

MGAAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGLIGKPSGKSKDCVFTEIVLENNYTAFQNAHREGWFMAFTROGRPRQASRSRQNRQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

### **Signal peptide:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 9-13, 126-130

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

### **Casein kinase II phosphorylation site.**

amino acids 65-69

### **Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

### **N-myristoylation site.**

amino acids 69-75, 188-194

### **Amidation site.**

amino acids 58-62

### **HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTTCTCCCTGTTGAATTTTGGCACATGGAG  
GACAGCAGCAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
CATTTTGATTTTGTCTGTTATTTTTTTTTTCTTTTCTTTTCCACCACATGTATTTTAT  
TTCGTACTTCAAAAATGGGCCTACAGACCACAAAGTGGCCCGCATGGGGCTTTTTCTCT  
GAAGTCTTGGCTTATCATTTCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCCTGCC  
CTAGTGTGTGCCCTGCGACAGGAACCTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG  
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATATG  
TGGATTCTCTGCAGAACTGCACAAATGTACAGTGGTGCACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCTCATGAACCTTCCCAAGAATGTACAGATTCTCCATTGTCAGGAAAAAC  
AATATTACAGCCATTTACGGGCTGCTCTTGGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACTCCATATCCACAGTGGGGGTGAAGACGGGGCTTCCGGGAGGCTATTAGCC  
TCAAATTTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCCTGTTGGGCTTCTCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAAATCGAATTGCTGTATATCCGACATGGCCCTCCAGAA  
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTGCTGTGCC  
CACCTCTCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGTCAGGACAACCCAGAT  
AAACCACATTCTCTTGACAGCTTCTCAAATCTGCGTAAGCTGGAACCGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCTTGGTTTTGTGACTGCAGTATTAATGGGTACAGAAATGGCTCAA  
ATATATCCCTTCATCTCTCAACGTGCGGGTTTTCATGTGCCAAGGTCCTGAACAAGTCCGGG  
GGATGGCCGTACAGGAATTAATATGAATCTTTGTCTGTCCACCAACGACGCCCGGCCCTG  
CCTCTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCACCCCTCTCTAT  
TCCAAACCTAGCAGAAGCTACACGCCCTCAACTCCTACCACATCGAACTTCCACAGATTCT  
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTCTGAACGGATCCAGCTCTCTATC  
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTCCACGGTGATGGCATA  
CAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTACAGGAGCCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGG  
CACCACCCATGCCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCAACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT  
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTCTGGCATATGCACAAAAGGGGCGCTACACCTC  
CCAGAAGTGGAAATACAACCGGGGCGGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACCTCATCTTGAGATGACAGAAACAGTTTTTCAGATCGTCTCTCTTAAATAACGAT  
CAACTCTTTAAAGGAGATTTTCAGACTGCAGCCATTACACCCAAATGGGGGCATTAAATTA  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCAGACCTTGAGGC  
ACTGCCATCGTGAACCCAGAGGCCAGCGTTATCAAGGCGCAATTAGACTCTTGAGAA  
CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT  
TTGTGCATTGGAATACCTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG  
CTATCTTTTCTATTTCAGTTAATTACAAACAGTTTTGTAACCTTTGCTTTTAAATCTT

## FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTVLVYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLLDDNSISTVGVEDGAFREAI SKLLFLSKNHLSSVPVGLFPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTCLKKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
PWFCDCSIKWVTEWLKYPSSSLNVRGFMCGPEQVRGMVRELNMMNLLSCPTTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPITPDWDGERVTPPISERIQLSIHFVND  
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNRAVEDTICSEATTHASYLNNGSNTASSHEQTTSMSGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQKWYKNGRRKDDYCEAGTKKDNSIEMTETS FQIVSLNNDDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

ACTTGGAGCAAGCGGGCGGCGGAGACAGAGGCGAGAGGCAGAAGCTGGGGCTCCGTCCTCGCCTCCCACGAGCG  
 ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCCAAGAGGCCGACGAGGAAGACCCCGGTGGCTGCGCCCCCTGCC  
 TCGCTTCCCAGGCGCCGCGGCTGACGCTTGGCCCCCTTGCTCGCCTTGAAATAGGAAAAGATGCTCGCAGGCT  
 GCTTTCTGCTGATCTCGGACAGATCGTCTCTCCTCGCTCCGAGGCGCAGGGAGCGGTACAGTGGGAGGTCATCT  
 CTAGGGGCGACACGCTCGGACCCACCCGCGAGCGGCCCTTCTGGAGAGTTCTGTGAGAACAAAGCGGGCGAGACC  
 TGGTTTTCATCTATGACAGCTCTCGCAGTGTCAACACCCATGACATATGCAAAAGGTCAAGGAGTTTCATCGTGGACA  
 TCTTGCAATTCTTGGACATTGGTCTGTATGTCAACCGAGTGGGCTGTCTCCAAATATGGCGAGCACTGTCAAGAATG  
 AGTTCTCCTCCTAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCAAGG  
 GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCGCGGCCCTGA  
 GGGAGAATGTGCCAGGGTCATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGCCGAGGTTGGCTGCTA  
 AGGCACGGGACACGCGGCATCCTTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG  
 GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAATTTCAGCGAGATTGAGACGCTGACCTCCGTGTTCC  
 AGAAGAAGTTGTGACGCGCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCACTTCTGCATCAACATCCCTG  
 GCTCATACGTCTGCAGGTGCAACCAAGGCTACATTTCTAACCTCGGATCAGACGACTTGCAGAATCCAGGATCTGT  
 GTGCCATGGAGGACCACAACCTGTGAGCAGCTCTGTGTGAATGTCCGGGCTCCTTCGTCTGCCAGTGTACAGTG  
 GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACCCAGGATGTGAAC  
 ATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCGAGTGCCATGAAGGATTGCTCTTAAACCAGATGAAAAA  
 CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT  
 ACTACTCGCCTGCCACCGCTGGCTACACTCTGGACCCCAATGGCAAAACCTCGAGCGAGTGGACCATCTGTGCAC  
 AGCAGGACCATGGCTGTGAGCAGCTGTGTGAAACACGAGGAGTTCCTTCGTGTCCAGTGTCTCAGAAGGCTTCC  
 TCATCAACGAGGACCTCAAGACCTGCTCCGGGTGGATTACTGCCCTGTGAGTGACCATGTTGTGAATACTCCT  
 GTGTCAACATGACAGATCCTTGCTGTGAGTGTCTGAGGAGACAGTGCTCGCAGCGATGGGAAGACGTTGTG  
 CAAAATTGGACTCTTGCTCTGGGGGACACGGTTGTGAACATTCGTGTGTAAGCAGTGAAGATTTCGTTGTGT  
 GCCAGTCTTTGAAGTTATATATCTCCGTGAAGTGGAAAAACCTCGAGAAGGAAGATGTCTGCCAAGCTATAG  
 ACCATGCTGTGTAACAGATTGTGTGAACAGTGAACGATGACGACTCATACAGTGCAGTGTGGAGGAGTTCCSGCTCG  
 CTGAGGATGGGAACCGTCCGGAAGGAAGATGTCTGCAATCAACCCACCTGGCTGCGAACAATTGTGTGTTA  
 ATAATGGAAATCTACATCTGCAAAATGCTCAGAGGATTTGTTCTAGCTGAGGACGGAACCGTGAAGAAAT  
 GCACTGAAGGCCAATTGCACTCGTCTTTGTGATCGATGGATCCAAGACTCTTGGAGAAGAGAATTTTGAAGTCG  
 TGAAGCAGTTTGTCTCATGGAATATAGATTCTTTGACAAATTTCCCCACGAGCCGCTCGAGTGGGCTGTCTCAGT  
 ATTCCACACAGGTCACACAGAGTCTACTCTGAGAAACTTCACTCAGCCAAAGACATGAAAAAAGCCGTTGGCCC  
 ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAAGAAAGTTTACCCAG  
 GAGAAGCGGCGACGCCCCCTTCCACAAGGGTGCACAGGACGCAATGTGTTCAACGCGAGCGGCTCAGGATG  
 ACCTCTCCAGTGGGCGAGTAAAGCCAGGCAATGGTATCACTATGTATGCTGTGGGGTAGGAAAAGCCATTG  
 AGAGGAACATACAAGAGATTGCTCTGAGGCCACAAACAAGCATCTCTTCTATGCGGAAGACTTCAGCACAAATGG  
 ATGAGATAAGTGAAAAATCAAGAAAGGACATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
 CAGGGGAACTGCCAAAAACCGTCCACAGCCAAACAGAAATCTGAGCCAGTCACCAATAATATCCAAGCCCTACTTT  
 CCTGTTCTAAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTACGGTCTACACAAAAGCTTT  
 TGGAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCAATGTATCACGGATTACAAT  
 GAACCGAGTCGAGAGCCCCAAGGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAAACATCAGTACTGA  
 GAAACCTGTTTGTGCCACAGAAACAGAGCAAGAAATATACATACTTTATCATGAAAAAATAATCCT  
 TCAGAATCTTAAGATGAATTTACAGGTGAGAATGAATAAGCTATGCAAGGATTTTGTAAATATACTGTGGACAC  
 AACTGTTCTTCTGCTCATCTGCTTGTGTGCAATCTATTGACTATGAGTAAAGTTTGCACAGTCTTACTT  
 CTGTAGAACAATGGCCATAGGAAATGCTGTTTTTGTACTGGAATTTTATACAATATTAATAATCCACCCTCAG  
 CATAAAATCATAGGACATATGTACTTGTGAAACAAGTTGGATTTTATACAATATTAATAATCCACCCTCAG

## FIGURE 15

MEKMLAGCFLILLGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFVIDILOFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KRMRLHSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTLSVFPQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCQLCVNVPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCINTRINYCALNKPGC  
EHECVNMEESSYCRCHRGYTLDPNGKTCRSVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLLI  
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPBGHVLRSDGKTCAKLDSALGDHGCE  
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCAIDHGCEHICVNSDDSYTCECLEGFRLA  
EDGKRCRRKDVCKSTHHGCEHICVNNNGNSYICKSEBGFVLAEDGRRCKKCTEGPIDLVFVID  
GSKSLGEENFEVVQKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEBELQRIASEPTNKHLYAEDFSTMDIESEKLKKGICEALEDSDGRQDS  
PAGELPKTVQQPTSESEPVTTINIQLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL  
EEKHDKQCKENLIMPQNLANEVVRKLTQRLEEMTQORMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC  
CATGATTTCCCTCCCGGGGCCCTGGTGACCAACTGTGTCGGTTTTTGTTCCTGGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACCTGCCCCCAACCGTTGCAG  
GCGGTGGAGGGAGGGGAAGTGGTGCTTCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTC'TCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC  
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT  
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCGCTCTCCAGGGTGTGCCCCAT  
GTGGGGGCAAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCTATCCGTG  
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGCCCTGGAGCTGC  
AGTGGTTGTCTGGAGCTGTTGTGGGTACCTGGTTGACTGGGGTTGCTGGCTGGGCTGGTCC  
TCTTGTAACACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCTGCCCTGGGCCAAGAGCTCAGACACAATCTCCAAGAAATGGGACCT  
TTCCTCTGTCACTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCCTGGTGAT  
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTCTTCTCTGGCTTGAGCCG  
CATGGTGCTGTGCCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATGATGAC  
CCCACCACTCATTTGGCTAAAGGATTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC  
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCAGTCACTGAGTCTCCAGGC  
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTGGGCTCCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTACGGCTGGCTTGGTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTC  
TTATTAAAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAAATTAATAAAGATACATAA  
TGTTTGTATGAAAAA



## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVFPVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLLEGLQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCTRLQGVPHVGANVTLSQCSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA  
VVAGAVVGTFLVGLGLLAGLVLLYHRRGKALEEPANDIKEDATAPRTLWPWKSSDTISKNGTL  
SSVTSARALRPPHPGPPRPGALTPTPSLSSQALPSPRLPTTGAHPQPIPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 245-267

### **N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

### **N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175



## FIGURE 19

MKRLPLLVPFSTLLNCSYTNQNTCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSSYYCMVPGFRSSSNQDRFITNDGTVCIEVNVNANCHLDNVICIAA  
NINKTLTKIRSIKEFPVALLQEVYRNSVTDLSPTDIIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTFVKTIVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSQFKTKTEFDT  
NSTDIALKVFFFDSYNMKHIHPHMNMMDGDYINIFPKRKAAYDSNGNVAVAFLLYKYSIGPLLS  
SSDNFLLPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF  
WNYSPTDMNGSWSSEGCCLTYSNETHTSCRNLHPTHFAILMSSGSPSIGIKDYNILTRITQLG  
IIISLCLCAICITFFWFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCFSIIAGL  
LHYFFLAFAWMCIIEGHIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVVGFSAALGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIYKVFRRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLVHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEYYRLFKNV  
PCCFGCLR

### **Signal peptide:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

### **N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

### **Glycosaminoglycan attachment site.**

amino acids 49-53

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

### **Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

### **Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

### **N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT  
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATTTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAAATAACATTACATTAAGTCATCGAAAGGTCACAGATAGGTATA  
GGAGTCTATGTGGCATTTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTACCTTC  
TGTTTCTTCAGTGAAATTCAAAGCACCAGGA

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## FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCTCTCCCGCAGATCCGAACGGCCTGGGCGGGGTCACCCCGGCTGGGA  
CAAGAAGCCGCCCTGCGTCCCGGGCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGCTTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGCCCGGAG  
CCGCCGCGCGTCAAGACGAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCC  
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTGTGGACTGCGCGCGGGG  
CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG  
CGTGACACAGCGTGGGTACCTCTGCATGGGCGCGGACGGCAAGATGCAAGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACCGCCTCCCGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCTGGAGACCGACAGCATG  
GACCCATTTGGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTAACT  
GAGACCATGCCCGGCCCTTCTACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG  
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA  
GTTGTACATATTAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT  
CATAAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCGTGGGCCCCATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACTCCATCGATGGGGAAC  
TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCAATTTTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
ACCATTGCGCTTCCCAAATCCCTCCAGGCCAGAAGTCACTGGAGCAGGCATGGCCCAACAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTCCTCC  
CTGAGGCCAGTTCTGTCTATGGATGCTGTCTTGAGAATAACTTGCTGTCCCGGTGCACTGTC  
TTCCATCTCCAGCCCCACCGCCCTTGCCACCTCAATGCTCCCATGGATTGGGGCCT  
CCCAGGCCCCCACTTATGTCAACCTGCACCTTCTGTTCAAAAATCAGGAAAAAGAAAGAT  
TTGAAGACCCCAAGTCTTGTCATAAATCTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC  
CCTTTCCCGCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA  
TCTCTTATTTCTTACATTATTTATGCCCCAAATATATTTATGTATGTAAGTGAGGTTTG  
TTTTGTATATATAAATGGAGTTTGTTTGT

**Figure 1**

Signal peptide:

Casein kinase II phosphorylation site.

N-myristoylation site.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

## FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCTCA  
GAGCAGCCGGCTGCCGCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCTCCTCCTGCTG  
CTGCTGCGTACCTGGTGGTCGCCCTGGGCTATCATAAGGCTATGGGTTTTCTGCCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCTGCAAAACCCCAA  
AGAAGACTGTTTTCTCCAGATTAGAGTGGAAGAACTGGGTCGGAGTGTCTCCTTTGTCTAC  
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG  
GATCAAAAATGTGACAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAAGGATGGCATCCGTTTGCTAGAAA  
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACTGGAAGT  
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTC  
TGTTGGATATCGCAGGTGTCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA  
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCAGCACTTTGGAAGG  
CCGCGCGGGCGGATCACGAGGTACAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC  
CATCTCTACTAAAATACAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGC  
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATA  
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

090393.07101

## **FIGURE 24**

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQQTQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQQNLEED  
TVTLEVLVAPAVPSCCEVPSSALSGTVVELRCQDKEGNPAPETWFKDGI RLL ENPRLGSQST  
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN SVGYRRC PGKRMQVDDLNI SGIIAAVVVVA  
LVISVCGLGVCYAQRKGYFSKETS FQKSNSSSKATTMSENVQWLT FVI PALW KAAAGGSRGQEF

### **Signal peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 130-144, 238-258

### **N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

### **Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

### **N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

### **Amidation site.**

amino acids 226-230





## **FIGURE 26**

MKDMPLRIHVLLGLAITTLVQAVDDKKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQIILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTLEPEKCLSELNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLLENLESISFYDNRL  
IKVPHVALQKVNVNLFKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSPIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICPLIAPESFSPNINV  
EAGSYVSFHCRTAEPPQPEIYWITPSGQKLLPNTLTDKFYVHSEGLDINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTA  
FVKTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVI CLISCLSPENMCDGGHSVVRNYLQKPTFALGELYPLIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

### **Signal sequence:**

amino acids 1-22

### **Transmembrane domain:**

amino acids 633-650

### **N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

### **Tyrosine kinase phosphorylation site.**

amino acids 570-579

### **N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

### **Cell attachment sequence.**

amino acids 277-280

## FIGURE 27

CCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC  
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAAACCGTTCCCTCTCCATGTGTCTCTCTACAAAGTTTGTTCCTTA  
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCTCTGGG  
GGTTTAAATGTACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCTCTCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGCACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC  
AACGTGATCTGTAAACGTCCTGTTGGATGAACATGCTGGCAGACCATTCCTCAATGCTGC  
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTTGGCTGGTTCATATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG  
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATTAGTGTCCAACTGACTGTCATTGAGAAAAGAAAGAA  
GTAGTTTGCATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA  
ACTTTGTATTTAGTTTTTTTTGAATTATGCCACTGCTGAACCTTTTAAACAACTACAACA  
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT  
AAGTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT  
AATTTAAAGCAAATAAAAGCTTAACCTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSSGGLNVTC SNANLKEI PRDL  
PPETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR  
IQSVHKNAFNNL KARARIANNPWHCDCTLQQVLRSMASNHETAHNVI CKTSVLDEHAGRPF  
NAANDADLCNL PKKTTDYAMLVTMFGWFTMVISYV VYVRQNQEDARRHLEYLKS LPSRQKK  
ADEPDDISTVV

### **Signal sequence:**

amino acids 1-33

### **Transmembrane domain:**

amino acids 205-220

### **N-glycosylation site.**

amino acids 47-51, 94-98

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

### **Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

### **N-myristoylation site.**

amino acids 37-43, 45-51, 110-116



## FIGURE 30

MQVSKRMLAGGVSRMPSPLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRRKF  
VAVPEGIPTETRLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL  
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTISIPTEALSHLHGLIVLRLRHLNINAIIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSIHNCNLTAVPYLAVRHLVYLRFLNLSYNPISITIEGSMLEH  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSGVGNLETILDSNPLA  
CDCRLLWVFRRRWRLNFRNQOPTCATPEFVQGEKFDPPDVLLPNYFTCCRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPEPAILWLSPRKHLVSAKSNGRLTVPDGTLEVRYAQVQDNGTYL  
CIAANAGGNDSPHAHLHVSYSYSPDWPQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCLVLLFLWSRGKGNKHNIEIYVPRKSDAGISSADAPRKFNMKMI

### Signal sequence:

amino acids 1-41

### Transmembrane domain:

amino acids 556-578

### N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

### Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

### Tyrosine kinase phosphorylation site.

amino acids 590-598

### N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

## FIGURE 31

CCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCATCCCCAGCCCCGGGGATTAGGCTCGCCAGCGCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGATGGGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTG  
TGTTCCGCTGTGCTGGGCGCCCGGGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCAAGTGC AAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCTAACCCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGTCTCAATCTTCACTATGCCTGT  
GCGAAGTGC AAGTCCCTCGTCACTGTGTCTAGGAATTCACAGAAGCCCATCATCACTGGTT  
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCTAAACTGTCACTCTCTGGGAGCAAG  
CCTGCAGCCCGGCTCACCCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCCAATGGTAAACCTTCACTGT CAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTTATACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTTCCCTTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG  
CAACATGGGCAGCTACAAGGCCTACTACACCTCAATGTTAATGACCCAGTCCGGTGCCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCCTGCTG  
CTCATCATGCTCATCTTCCCTTGGCCACTACTTGATCCGGCACA AAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGTCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGGCG  
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTAGAGGCGCTGCCCACTTCTCTGC  
GCCCCCAGGGGCCCTGTGGGGACTGTGGGGCCGTACCAACCCGGACTTGTACAGAGCAA  
CCG CAGGGCCGCCCTCCCGCTTGCTCCCCAGCCACCCACCCCTGTACAGAATGTCTGC  
TTTGGGTGCGGTTTTGTACTCGGTTTGG AATGGGGAGGGAGAGGGCGGGGGAGGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTTCTCTGCATTGGGTTATTATTAATTTTGTAAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA  
AACAAAAACA

## **FIGURE 32**

MGAPAAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRILQVTSTPHELSSISINVALADEGEYTCSIFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTRREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLHCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YITLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGYTLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 331-352

### **N-glycosylation site.**

amino acids 25-29, 290-294

### **Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

### **N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



**ORDER OF THE**

GGGGGTTAGGGAGGAGGAAGTAATCCACCCCCACCCCCCAAACCTTTTCTTCTCCTTTCTCGTGTCTTCGGACATTTGAGACGACAAATGAACCTGAATGTGTCTGTGGCGGAGCAGGATGGTCTGCTGTTACTTTGTGATGAGCATCGGGAGTAATGCTCGCTGTAAAAATGCTGCTTTGGATTTCTGTTGCTGGAGACGCTCTCTTTGTTTTCGCCGTGGAACGTTACAGGGGACGTTTGCAAAGAGAAGA CTGTTCTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACAAGTCTGCAGCGTTTACATGCCCGACATCCCGAGTTTACCATTTATTTCTGATGTCGCAATTCCTCCTACGACTTTCCTCCATAATGAGTTCGCTAACTTTTATAATGCGGTAGTTTGCACATGGAAAAACAATGCGTTTGCATGAAATCGTTCCGGGGCTTTCTGGGGCTGCAGCTGGTGAAAAAGCTGCACATCAACAACAACAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGATCTGGAATATCTCCAGGCTGATTTTAAATTTATTACAGAGATATAGACCCGGGGGCTTCCGAGACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAACTCATCAGACCTCATGCTGCCAACTGTGTTCCAGTATGTGCCATACCCCACTGACCTCCGGGGTACAGGCTGAAAAAGCTGCCCTATGAGGAGGCTTGGAGCAAACTCCCTGGTATTTGGCGGAGATCTCGTAGAGGATAACCTTTGGGACTGCTGTGATCTGCCTTCCCTGAAAGAATGGCTGAAAAACATTTCCAAGAATGCCCTGTACTCGGGCGAGTGGTCTGCGAAGCCCCCACTGACAGCTGCAGGGTAAAGACCTCAATGAAACACCCGAAACAGGACTTGTGCTCTTTGAAAAACCGATGGATTTAGTCTCCCGCGGCCCTCTGCCAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAGAGGATCATGCGCACACAGGGGTCTGCTCCAAAGCGGAGTACAAAGATCCGAGCAACTGGCAGATCAAATACAGCCACAGCAGGCATAGCGACGGGTAGCTCGAGGAAACAAACCTTAGCTAACA GTTTTCCCTGCTCCGCTGGGGCTGCAGCTGCGACACATCCCAAGGCTGGGTTTAAAGATGAAGTGAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTCAAGCTGCAGAGCTTTTCTACGAGATAACAAGATCCACAGATCCGAAATCGCACTTTGTGGATTACAAGAACCTCACTGTTGTGATCTGGGCAACAATAACATCGCTACTGTAGAGAAACAACATTTTCAAGAACCTTTTGGACCTCAGGTGGCTATACGTGTAGATGCAATTAAGCTGGACAGCTGCCCGGAGAAATTCGCGGGGCTGCAAAACCTAGAGTACTGAAACGTGAGATCAACAGCTATCCAGCTCATCTCCCGGGCACTTTCAATGCCATGGCCCAAACCTGAGGATCCCTATTCTCAACAACAACCTGTGAGGTCCCTGCTGTGGACGTGTTCGTGGGGTCTGCCTCTTAAACTCAGCTGCACAAACAATTACTTCATGTAACCTCCGGTGGCAGGGGTGCTGCACAGTTAACTCCATCATCGCATAGACCTCCAGGAAACCTGGGAGTGTCTCTGCAATTTGTCCTTTCAAGCAGTGGCGAGAACGCTTGGGTTCGGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGTGAACTTCTTGTAGAAAGATTTTCATGCTCTCTCCATCAATGACAGATCTGCCCTCAGCTGTACGCTTAGGATCTCGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTGGCGGACCGGACGCGACATCCAACTCTACCTAGACACAGCAGGAGTTCATCTCGGTGTGTGTCCTCGGGGACTGCTGCTGGTTGTTTCCCTCACTCCGCTTACCGTTCACCGTGGTGGCGATCTCTCGCTCGCGCTCCGAGATTAATTCCTACAGACAGTCTGTGACTCTTCTCATTTGGCCAAATTTGGGCTTCAACAGCACTGGGGCGCCAGAGTGATGACTGTGGCTCTACGCTCTCAGACTAAGACCTCAACAGCCCAATAGGGGAGGGCAGGGTGAAGCGCATACATCCTTCCCCACCGCAGGCACCCCGGGGCTGGAGGGGCGTGTACCAAAATCCCGCGCCATCAGCTGTGATGGGCTAAGTATAGTATATAATCTGTAGCTTGCAGTCTGCACAACTGAGCTGCGACAACTGGGAGCTGGGAGGGCGCAGCCAGCTGAGCTGCTCTTTGTGTGAGACCCCTTTTGGGACAGCCCTTTTGGGACAAAGCCGACAGCCGCTGCTGTGAAGAACTGACAGTGCCTCGCCCTCGCGCTCGCGCTGTTGGATTTGGATTCAGCTGCTATATATACATATATCCATCTATATAGAGAGATAGATATCTATTTTTCCTCTGGATTAGCCCGGTGATGGCTCCCTGTGTGCTTGGCTCAGCGAGGATGGGCAGTTTGCACGAAGCACTGAATGTATGTGATAAAGTAACTTTGACTCTTCGAC

## FIGURE 34

MLLWILLETSCLFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLPNEFANFYNAVSLHMENGLHEIVPGAFLGLQVLKRLHINNKKISFRKQ  
TFLGLDDLEYLQADFNLRLRIDPGAQDLNKLEVLILNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPIYEEVLEQIPGIAEILLEDNFWDCCTCDLLSLKEWLENI PKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPKKNRVDSLLPAPPAQEETFAPGPLPTPFKTNQEDHATPGSAPNGGK  
IPGNWQIKIRPTAAIATGSSRNKPLANS LCPGGCSCDHI PGSGLKMN CNRRNVSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLDDLRLWLYMDSNY  
LDTLSREKFAGLQNLLEYLNVEYNAIQLILPGTFNAMPKRLRILILNNLLRSLPVDVFAGVSL  
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSI SVL  
VPGLLLVFVTSAFTVVGMLVFILRNKRKSKRRDANSSASEINSLQTVCDSSSYWHNGPYNADG  
AHRVYDCGSHSLSD

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 618-638

### **N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

### **Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

### **N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## FIGURE 35

AGTCGACTGCGTCCCTGTACCCGGCGCCAGCTGTGTTCTTGACCCAGAAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAAACTGTTGGC  
CGCTGGGCCCCGCGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCTTCGAGCGGGACAGATCCAAAGTTGGGAGCAGCTCTGCGTGCAGGGGCGCTCAG  
AGAAATGAGGCCGCGTTCGCCCTGTGCCCTCTTGGCAGGCGCTCTGGCCCCGGGC CGGGCGG  
CGGCGAACACCCCACTGCCGACCGTGTCTGGCTGTCTGCGCTCGGGGGCCTGCTACAGCTGCG  
ACCACGCTACCATGAAGCGGCAGGCGGCGAGGAGGCTGCATCTCTGCGAGTTGGGGCGCTC  
AGCACCGTGCCTGCGGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCCAGG  
GCCCGGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCTCACT  
GCACCTTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGGCGGTCTC  
GAAAGCGACACGCTGCACTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTGCAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCCTGCGCCGCGCCCCGGG  
GCCGCTCTTAACTTGAGCTATCGCGCGCCCTTCAGCTGCACAGCGCGCTCTGGAATTCAG  
TCCACCTGGGACCGAGGTGAGTGCGCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTGCA  
TCGCGGACGAAATCGGCGCTGCTGGGACAAACTCTCGGGCGATGTGTTGTGTCCTGCCCC  
GGGAGGTACCTCCGTGCTGGCAATGCGCAGAGCTCCTAACTGCTAGACGACTTGGGAGG  
CTTTGCGCTGCAATGTGCTACGGGCTTCGAGCTGGGGAGGACCGCGCTCTTGTGTGACCA  
GTGGGGAAGGACAGCCGACCTTGGGGGACCGGGGTGCCACCAGGCGCCGCGCGGCCACT  
GCAACCAGCCCCGTGCCGACAGAGAATGGCCAACTCAGGGTCGACGAGAAGCTGGGAGAGAC  
ACCACTTGCTCCCTGAACAAGACAATTCAGTAACATCTATTCTGAGATTCTCGATGGGGAT  
CACAGAGCAGATGTCTACCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCTCTGCACTCTCAGGCTTT  
CGACTCCTCTCTGCGCGTGGTCTTCATATTGTGAGCAGCAGTAGTAGTGTGTTGGTGATCT  
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCAAGAAAGCCCTCTTCCCAGCCA  
AGGAAGGAGTCTATGGGCCCCCGGGCCTGGAGAGTGATCTGAGCCCGCTGCTTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCTTTGCTGGCGGAGTCCCCCTTGGCTCTAGTGATGCATAGGGAACAGGGGA  
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTAC  
TTGTGTAACGACAATTTCTGCAGAAATCCCCCTTCTCTAAATCCCTTTACTCCACTGAG  
GAGCTAAATCAGAAGCTGCACACTCCTTCCCTGATGATAGGGAAGTGAAGTGCCCTTAGGA  
TGGTGATACTGGGGGACCGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGGAGAA  
TTTGAGAAAGTGATTGAACTTTTCAAGACATTGGAACAAATAGAACACAATATAATTTACA  
TTAAAAAATAATTTCTACCAAAATGGAAGGAAATGTTCTATGTTGTTTCAAGGTAGGAGTAT  
ATTGGTTCGAAATCCAGGGGAAAAAATAAAAAATAAAAAATTAAGGATTGTTGAT

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## FIGURE 37

CGGACGCGTGGGATTACAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAACTAAG  
 CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAGTGCCTCCGCCCTGCGGGCCGCGTATC  
 CCCC GGCTACTGGGCCGCCCCCGCGCGGTGCGCGCTGAGAGGGAGCGCGCGGGCAGCCGA  
 GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGTGCGGA  
 GGGCGGTGTGTGCCGGCGCGCGCCGTGGGGTGCAAAACCCGAGCGCTACAGCTGCC**ATGA**  
 GGGGCGCGAAGCGCTGGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG  
 CAGCAGTCCCCAGAGAGACCTGTTTTCACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
 TATTGGCAGTGAAGGTTTTCCTGGAGTGTACCCTCCAAATAGCAAAATGTACTTGGAAAATCA  
 CAGTTCGCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTCTAGACCTCGAGAGTGACAAC  
 CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTTGGCCG  
 CTTCTGTGGCACTTTCGGCCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
 TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA  
 AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC  
 CCCCAACTGGCCAGACCGGGATTACCTTGCGAGGAGTCACTTGTGTGTGGCACATTGTAGCCC  
 CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC  
 CGATATGATTATTGTGGCTGTGTTTAAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA  
 GTATTGTGGTGATAGTCCACCTGCGCCAAATGTGTCTGAGAGAAATGAACCTCTTATTTCAGT  
 TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTAGGCCAAAA  
 AAACCTGCCTACAACCTACAGAACAGCCTGTCAACCACCACATTCCCTGTAAACCACGGGTTTAAA  
 ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT  
 GTTCAAGTGACTTTGTATTAGCCGGCACGTGTATCACAAACCATCACTCGCGATGGGAGTTTG  
 CAGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTTCAGCAGGCGGG  
 CAAGAACATGAGTGCCAGGCTGACTGTGCTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC  
 TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCCAAATCATGCCAACAGC  
 TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAATAAGCAATG  
**TTAA**CAGTGAACCTGTGTCCATTTAAGCTGTATTCTGCCATTGCCCTTTGAAAGATCTATGTTT  
 TCTCAGTAGAAAAAAAATACTTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAAGATGG  
 GACTGGTTGACTCTTCATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAAGTTCTT  
 TGCCTGCTGTACAGGAGCAGCTATCTGATTGGAACCTGCCGACTTAGTGCGGTGATAGGA  
 AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTATACATCTCTGTAAAAGGAT  
 ATTTTGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTTATAGT  
 GTTATTGTTTCAAGCCTTTGCCCTGAGGTGTACAATCTGTCTTGCCTTTTCTA  
 AATCAATGCTTAATAAAATATTTTAAAGGAAAAAAAAAAAA



[illegible]

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGGGCTGGGGCGGTGCTTCTTCTTCTTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCATGGCCCCGGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCAGTCTTCTCCCCGCTCAGCCCCATCGTGTCTATACCTG  
CCGGGACTGGTTGACAGCTTTAACAGGGCCTGGAGAGAACCATCCGGGACAACTTTGGAG  
GTGGAAACACTGCTGGGAGGAAGAGAAATTGTCCAATACAAAGACAGTGAGACCCGCGCTG  
GTAGAGGTGCTGGAGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCTGTGGAGCT  
GAGTGAGGAGCTGGTGAGAGCTGGTGGTTTCAAGCAGCAGGAGGCCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTTCGGGCCCTCTGTC  
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCTGTGGCC  
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCTCTGGTATCTTGGCTGTG  
TTTGGCCCTGTGCCCGATGCTCAGGACTCAGGAGTACCAACTGTTTTCAGTGCAGAAAGG  
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATGTAGAGTGTGGCAGAGGGGACCAACT  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCTGTGAAGAAGTGTAGCCCTGGCTATCA  
GCAGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCAGGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACGCGCATCTTCATTGGGGCTGTGGCGGCCATG  
ACTGGCTACTGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCACTGTAGGACCTCCTCCCACCCACGCTGCCCCAGAGCTTGGGCTGCCCT  
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTGTAGAGTGGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTTCACTGGCGGGGACTGGCAGGCTTCACATGTGTGA  
ATTTCAAAGTTTTTCTTAAATGGTGGCTGCTAGAGCTTTGGCCCTGCTTAGGATTAGGTG  
TCTCTCACAGGGGTGGGGCATCACAGCTCCCTCTGCCAGTCGATGCTGCCAGTTCCTGT  
TGTCTTGTACCATCCCCACCCCATTTGCCATTATTATTATCATCTCAGGAAATAAAGA  
AAGGCTTTGGAAGTTTAAAAAATAAAAAAATAAAAAA

## **FIGURE 40**

MAPWPWKGLVPAVLWGLSLFLNLPGPPIWLQSPPPQSSPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWBEENLSKYKDSERLVEVLEGVCSKSDFECHRLLLESEELVESWWFHKQ  
QEAPDLFWLCSDSLKLCCPAGTFGPSCLP CGGTERPCGGYGQCEGEGTRGGSGHCD CQAG  
YGGEACGQCGLGYFEARNASHLVCSACFGPCARCSGPPEESNCLQCKKGWALHHLKCV DIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVLVQQMFFG  
IIICALATLAAKGLDVLFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

### **Signal sequence:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 372-395

### **N-glycosylation site.**

amino acids 79-83, 205-209

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

### **Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

### **N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

### **EGF-like domain cysteine pattern signature.**

amino acids 181-193



## FIGURE 41

TGAGACCTCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT  
GCCCCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCACT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGTCCCGCGGAAAGAGGTTTCAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTTCCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCAGG  
AGCCCGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCGGGCC  
CGGGTGACCGTTCGAGTGGCTGCGCTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGACAGG  
GAGCATCTGGGCCCCGTGGCGTCCGGCGCCCAAGCTGGTCCGCTTTGCCCTGCAGGGGGC  
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG  
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAAGTGGGTGCTGGAGCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTCAAGTGGC  
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATTAGCGCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTTCAGGGTACCAGGAGAGCTG  
GCGATGACTGAAGTGTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT  
CCTCTGACAAAGTTACCTCACCTAATTTTGTCTCTCAGGAATGAGAATCTTTGGCCACTGGA  
GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCACATATATTCTAAGCACTTACAT  
GTGGAGATACTGTAACTGAGGGCAGAAAGCCANTGTGTATTGTTTACTTGTCTGTGCAC  
TGGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAAAATGAATAAAACACATTTTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFSQSFREYAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAAALHRHGRSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTAVNF  
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDGCDPEAPMTGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWP  
LGPRQCIASETDSLPMIVSIKEGGTRTPQVVSLPNMRVQKCSASDGAIVPRLQP

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 158-162

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

### **N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

### **Amidation site.**

amino acids 74-78

### **TGF-beta family signature.**

amino acids 282-298

## FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCG**AT**GGGGACAAA  
 GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG  
 CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT  
 GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTCTCCCGTGTGGAGTGGAAGTTTGACCA  
 AGGAGACACCACAGACTCGTTTGTCTATAATAACAAGATCAGACCTTCCTATGAGGACCGGG  
 TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
 ACTTGATATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
 GCTTGTGCCTCCATCCAAGCCTACAGTTAACAATCCCCCTCCTCTGCCACCATTGGGAACCGGG  
 CAGTGCTGACATGCTCAGAACAAGATGGTTCCTCCACCTTCTGAATACACCTGGTTCAAAGAT  
 GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT  
 GAATCCCAACACGAGAGCTGGTCTTTGATCCCTGTGAGCCTCTGATACTGGAGAATACA  
 GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT  
 GTGGAGCGGAATGTGGGGTTCATCGTGGCAGCCGTCTTGTAAACCTGATTCTCCTGGGAAT  
 CTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGGA  
 CTTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG  
 ACCTCGTCATTCTGGTG**TGAG**CCCTGGTTCGGCTCACCGCCTATCATCTGCATTTCGCTTACT  
 CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTC  
 TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTGAGCTATGTGCCCC  
 ATCTCCTTCATGCCCTCCCTCCCTTTCCTACCACTGCTGAGTGGCCTGGAACCTGTTTAAA  
 GTGTTTATTTCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
 TTCTAAGTAGACAGCAAAAATGGCGGGGTTCGAGGAATCTGCACTCAACTGCCACCTGGC  
 TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTCCCTTGTTACTGAC  
 GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGCTGAAATGGTTGTTGG  
 TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG  
 CCACCTGGGATCCCTCTGCCCTGTCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT  
 GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTTCAGAGAACTTGAAGCCAAAAG  
 GATTTAAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG  
 TAATCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTGGGATCAGCCTGACCA  
 ACATGGAGAAACCCTACTGGAAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
 CCAGCTGCTCAGGAGCTGGCAACAAGAGCAAAAACCTCCAGCTCAAAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRI PENNPVKLS CAYSGFSSPRVEW  
KFDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGT YTCMVSEEGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGI VMPTNPKSTRAFSNS  
SYVLNPTTGELVDFPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVA AVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 238-255

### **N-glycosylation site.**

amino acids 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

### **Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

### **N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262



## 0712

Signal sequence:

Transmembrane domain:

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

## FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG  
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGTAAGTCGATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGATATCATGGAATGAACCCGAGCAATG  
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCAGGGGCGGGTT  
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTCTACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA  
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA  
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTCATGAAGGATTCAGATCCGG  
TACCCCGACCTACACAATATGGTTTTATTATGTGCGGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAACATCTCTGAGC  
TCCAGACCTCCTTCCCGGTGGGACTGTGATCTCCTATCGTGCTTCCCGGATTTAAACTT  
GATGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCACCCCGGTG  
CCTTGCTCTGGAAGCCCAAGCTGTGCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGTCT  
GCCACCCGCGCCCTTGTGAGCGCTACAACCACGGAAGTGTGGTGAGTTTTACTGCGATCCT  
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTTCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCTGAGACCTCCTGA  
CCACGTGGAAGATTGTGGCGTTTACGGCAACCAGTGTGCTGCTGGTGCTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTCCCCCAGGGGGCCTCCCCGGAG  
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTCTATG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG  
GGCTGCCCTTACCCGTGGACGACCCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA  
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA  
GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCACCCCTGCTTCGGACAACCTTGACATA  
ATTGCCAGCAGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCATCATGCCACTGGGT  
GTTGTTCTTAAGAAACTGATTGATTAAAAAATTTCCCAAAGTGTCCTGAAGTGCTCTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCCTTCTCTCTTGGTTTTAGACAAATGTAAACAA  
AGCTCTGATCCTTAAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC  
CTGTTTCTTCTTGACACAGACTGATTAAAAAATTAAGNAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFCLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSPPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFATSVLLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDPPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQCPLFVDDQSPPAYPGSGD TDTGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFRLN

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 325-344

### **N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

### **Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

### **N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405



## FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCCGTGGCCCTAGAGA  
TGCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCCTCTGCCCGCCAGCCCGCTCCACCGCCGT  
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG  
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC  
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTTA  
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA  
AAGTTCAATTGAAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCAGACCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT  
CACAATTTAGGAACTGGTATGTGGATGAGCCGCTCTGCGGCAGCGAGGTCTGCGTGGTCA  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCCCTACATGTTCCAGTGAATGATGA  
CCGFTGCAACATGAAGAACAATTTCAATTGCAAAATATCTGATGAGAAACCAGCAGTTCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG  
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCGTTGAATCTGGCCTACAT  
CCTAATCCCAGCATTTCCCTTCTCCTCCTCTGTGGTCACCACAGTTGTATGTTGGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAAGCAACACACCATC  
TGCCCTCTCCTCACCAGGGAACAGCCCGACCTAGAGGTCTACAATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT  
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGTGGATTGTGACCAATGACATTTATGA  
GTTCTCCCCAGACCAATGCGGGAGGAGTAAGGAGTCTGGATGGGTGGAATAAGAAATATATG  
GTTATTAGACATATAAAAACTGAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC  
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCTGT  
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTGGCTGTATCCTTTAT  
CCCAGCCAGTCAATCCAGCTCGACCTTATGAGAAGGTACCTTGCCCGGTCTGGCACATAGTA  
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG  
CAGCATATATTATCATACAGACAGAAAAATCCAGAATCTTTCAAAGCCCATATGGTAGCACAG  
GTTGCCTGTGCATCGGCAATTTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRLGGQPVCRRGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSI ESEDEQK LIEKF IENLLPSDGD F WIGLR RREKQSNSTACQDL  
YAWTDGSI SQFRNWYVDEP SCGSEVCVVMYHQPSAPAGIGGPFYMFQWNDDRCNMKNNFICKY  
SDEKPAVP SREARGEETELTTPVLPEETQEEDAKKTFKESREAA NLAYILIPS IPLL LLLLV  
VTTVCVWVWICRKRKREQPD PSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETR PDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSES GFVTLVSVESG FVTNDIYEFSPDQMGRSKES  
GWVENEIYGY

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 117-121, 312-316

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

### **Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

### **N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGTCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCTCTCTGCAGCCTCAACCCGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTCAGCATGCGTTGTGGACCCAGTGCGGCGTCCTGACCTCGCTGGCGTACTGCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC  
CTGCTGAAGTTGAAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACCTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCTGAAGGGGGCATGTTTGTGGGCAGCTGACCAAGGTGGGCAT  
GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC  
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTGTTTCCACTAACATTTTCGGAATCTG  
GAGTCCACCCGTTGTTTGTCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTGAGAACTCTTGATCCCCAACTACCAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAGAGGCCGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG  
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGAATTCTTCATCTCCT  
GGACAACTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG  
CAGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCATTCTCCACATCTTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGTACCACAAATGGCCACCGTTTGTCT  
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGTCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT  
TCTTGAATGCCATGTGAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTATATAAAGCAGGATGTGTTGATT  
TTAAAATAAAGTGCCCTTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCFVDRSLLKLMVQVVFRRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMPAGQL  
TKVGMQQMPALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFCQCKE  
GPIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKVKKDRMGIDSSDKVD  
FFILLDNVAEQAHNLPSCPMLKRFRARMIEQRAVDTSLYILPKEDRESLQMAVGPFPHILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSPKEYHALCSQTQVMEVGNEE

### **Signal sequence:**

amino acids 1-23

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

### **Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

### **Tyrosine kinase phosphorylation site.**

amino acids 280-288

### **N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

### **Amidation site.**

amino acids 216-220

### **Leucine zipper pattern.**

amino acids 10-32

### **Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

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CTCTCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT  
TAAATTTTCAGCTCATCACCTTACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTTGCACCAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACC GTGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTGTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG  
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCAGAGAGCTCTTTCTCCCCA  
GTCCACAGAGGGTGTCAAGCTGGCTGACGGCCCTGGGCATTGCAAGGACGCGTGGAAAGTGAA  
GCACCAGAAACAGTGTGATACCGTGTGCCAGCAGGCTGGAGCCTCGGGCCGCAAGAGTGG  
TGTGCCGCGCAGTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGTGCAACAAGCATGCC  
TATGGCCGAAAAACCATCTGTGCTGAGCCAGATGTGTCATCTCAGGACGAGAAGCAACCCCTTCA  
GGAATGCCCCCTTCTGGGGCTTGGGGGAAGAACACCTGCAACCTATGATGAAGACACGTGGGTG  
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGTCTTGGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA  
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCACTGTCTCAGTGTTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCCTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCCTCAGGCCATCAGACATAGTTTGGAACTACATCA  
CCACCTTTCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCATTGTCTCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA  
TTCATGAAGACCGAAATTTTAAGGATAAAATTTCTGAATTGGTTATGGGGTTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATCTCGTGAACCTTATTTTACAATAATAAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPSGVRLVGGGLHRCGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGILYEPPEAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC  
ENPESFSFPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEV LHKGVWGSVCCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

### **Signal sequence:**

amino acids 1-15

### **Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

### **N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

### **Amidation site.**

amino acids 196-200

### **Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

**0907-07**

ACTGCACTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTTCATCACTCCACAGCCATCTCGCCCTGCTGTTTCGGCTGCCTGGG  
CGTCTTCGGCCTCTTCGGGCTGCTGCAGTGGGTGCGCGGGGAAGGCCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCTCTGCAGTGCCTTTGGCTATGT  
GACATCTTGTCAACAATGTGGGATCAGCTACCTGTGATACCTGCAGACACCAAGCTGGA  
TGATGACAAGAGGTCTAGGAGACAACACTTCTTGGCCAGTTGCTCTAACGAAGAGCACTTC  
TGCCCTCATGATCAAGAGGAGGCAAGGCCACATTTGTGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA  
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGCCCGAGGATGTTCTTGTCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTATCTTCGAA  
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGACGCGAAATCC  
AAGAACTCTTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC  
TTACTCTACAAGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTGTCTCACAAGTGGG  
AAAGACTGAAGAAACACATCTCGTGAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA  
AGCTTCTCTCCAGGTTGAGGGGCAAAACACTTAAGGAATAAATATGAGCTGGGTTTAAACAT  
AAAAACTAGAAATAATACCTCAACAGCTAAAGAAAAAAGGCGCGCGCACTTAG  
AGTCGACCTGCAGAAGCTTGGCGGCATGGCCCAACTGTTTATTCAGCTTTAATATGGTTA

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVTGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAEBILQCFGYVDIL  
VNNAGISYRGTIMDTTVDVDRVMEETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQKMSI  
PFRSAYAASKHATQAFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 104-120, 278-292

### **N-glycosylation site.**

amino acids 228-232

### **Glycosaminoglycan attachment site.**

amino acids 47-51

### **Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

### **Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

### **N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

### **Amidation site.**

amino acids 265-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17



**FIGURE 57**

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA  
AAAAAAAAACACACCAAACGCTCGCAGCCAAAAAGGGATGAAATTTCTTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTCTAA  
GAGGAGAAAATCAGTCACCGCGGCAAAATCGTGTGATTACAGGAGCTGGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTTGTCTAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGACTGGGTGCCAAGGTTCATACCTTTGT  
GGTAGACTCGAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA  
GGCATTTCCTTCGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG  
CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA  
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG  
TCTGTGTCCTAATTTCTGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG  
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATGGAAGGATCCCTCCTGAGCGTTT  
CCTGGCAGTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAATTAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCTCTA  
ATAGTGCCAGAATTTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA  
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTGTTCCTTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA  
CCAAATGACTTTATTAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA  
AATTTGTACCATAACCGTTTATTTAACATATATTTTATTTTGTATTGCACTTAAATTTTGT  
ATAATTTGTGTTTCTTTTCTGTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA  
TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACCTCTCAATGGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA  
AA  
AA

## **FIGURE 58**

MKFLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTASAAGHVSVPFLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

### **Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

### **N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

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## **FIGURE 60**

MVGAMWKVIVSLVLLMPGFCDGLFRSLYRSVSMPPKGDGSGQLFLTPYIEAGKIQKGRELSL  
VGFPFGLNMKSYAGFLT VNKTYNSNLFFWFPPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLRDRDFPWTTLTSLMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALI QF  
FQIFPEYKNNDFVVTGESYAGKYVPAIAHLIHS LN PVREV KINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHBCIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNV TG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKFWLT  
EIMNNYKVLIYNGQLDIIVAAALTE RSLMGMDWKGSQ EYKKA EKKVWKIFKSDSEVAGYIRQ  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPPYVG

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

### **Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

### **Tyrosine kinase phosphorylation site.**

amino acids 423-432

### **N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

### **Serine carboxypeptidases, serine active site.**

amino acids 200-208

### **Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAACAT  
TTTTCCCTTTCTTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCACTCCTTG  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAATAGGAAGGAATTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGGAGGGCTTGCCTAACAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGGAAAGACTGGGTTTGTCTTAATATCAAAATGACTGGCTGGG  
TGAACCTTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTTGTAAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCTGAACATTCTTAAGAGGGAGAAAGTATGTTAAAAATA  
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCTGGGTC  
AGGCCAGCCTCTTTGCTCTCCCGAAATTAATTTTGGTCTGACCCTCTGCTTGTGTTTT  
GCAGAATCATGTGAGGGCCAAACCGGGGAAGGTGGAGCAGATGAGCACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGGCCTGGAGGTGG  
ACAGCCGCTCTGTGGTCTGTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC  
ATGCCCTCAGTTTCAGCACTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACCTTGACCGT  
CCACCAAGGGACGGGGCCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG  
CCCCTCATCTGTGAGCCCTGCAGCGAAGTGCTCACCTTCAACCAATGTCAACAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCTGTGTGGCTGTGGGAGCCTCTACCAGGGGTCTGCA  
AGCTGTGCGGCTGGATGACCTCTTCATCTGTGGTGGAGCCATCCCAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCCTGCCA  
GCCGGAAGCTGCCCGAGACCTTGAGTCTCAGCATGCTCGACTATGAGATACACAGCGAT  
TTTGTCTCTCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGGTCTCCCACTTTGACAT  
CTTCTACATCTACGGCTTTGTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCAGCATCTGTGCGG  
CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCGCTTCGGCTGCACCCGGGC  
CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC  
AGGCCCTCAATATCACAGGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAAGGGCAGAAG  
CAGTATCACCAACCCGCCGATGACTCTGCCCTGTGTGCCCTTCCCTATCCGGGCCATCAACT  
GCAGATCAAGGAGCGCCTGCAGTCTTGCTACAGGGCGAGGGCAACTGGAGCTCAACTGGC  
TGCTGGGGAAGGACGTCCAGTGACAGGAAGGCGCTGTCCCCATCGATGATAACTTCTGTGGA  
CTGGACATCAACAGCCCTCGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCCTCTACGTTTACAACGGCTACAGCGTGGTTTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTGAGATGCTCCAATGCC  
ATTCACTCTCTCAGCAAGAGTCCCTCTTGGGAAGGTAGCTATTGGTGGAGATTTAACTATAG  
GCAACTTTATTTCTTGGGGAAACAAGGTTGAATGGGGAGGTAAGAAAGGGGTTAAATTTGTG  
ACTTAGCTTCTAGTACTTCTCTCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA  
TTTCAATATTTCCCAAACCTTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAA

## **FIGURE 62**

MGTLGQASLFAPPNGYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVLLSVVWVLLAPPAAGMPQFSTFHSENDRDWTFNHLLTVHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL  
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGQDY  
FPTLSSRKLPDPRESSAMLDYELHSDVFSSLIKIPSDTLALVSHFDIFYIYGASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFAIFSKGQKYHHPDDSALCAFPPIRAINLQIKERLQSCYQGEEN  
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLKKVRVYEFRCNSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

### **Signal sequence:**

amino acids 1-32

### **Transmembrane domain:**

amino acids 71-87

### **N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

### **Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

### **N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

# FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGGGACTGGAGTGGGAACCCGGGCTCCCGCGCTTAGAGAACACGCGATGACCA  
 CGTGGAGCCTCCGGCGGAGGCCCGGCCGACGCTGGGACTCTCTGCTGCTGGTCTGCTTTGGGCTTCTCTGGTCTCC  
 GCAGCTGGACTGGAGACACCTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGAGGCCAAGGGCTGGA  
 ACTTCATGCTGGAGGATTCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCGCTGTGCCAGGGGACT  
 GGAGGGACCGCTGCTGAAGATGAAGGCTTGGCTTGAACACCTCACCACTATTGTTCCGTGGAACCTGCAATG  
 AGCCAGAAAGAGGCAAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCTTCGCTCTGATGGCCGACAGAGATCG  
 GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCACTGAGATGGACCTCGGGGGCTTGGCCAGCTGGGCTAC  
 TCCAAGACCTGGCATGAGGCTGAGGACAACCTTACAAGGGCTTCCACGAAGCAGTGGACCTTTATTGAGCAACC  
 TGATGTCCAGGGTGTGTGCCATCCAGTACAAGCGTGGGGGACCTATCATTTGCCGTGAGGTGGAGAAATGAATATG  
 GTTCTTATATAAAGACCCGACATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACTGTC  
 TCTGACTTCAGACAACCAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTGGCCACCATCTGCTGCACT  
 CAACAACAGGCTGACGCTACTGACCACCTTTCTCTCAACGTCCAGGGGACTCAGCCCAAGATGGTATGGAGT  
 ACTGGACGGGGTGGTTTGACTCTGTTGGGGAGGCCCTACAATATCTTGGATTCTCTGAGGTTTGAAGAACCGTGT  
 CTGCCATTGTGGAGCCGGCTCTCCATCAACCTCTACATGTTCCAGGAGGACCAACTTTGGCTTCATGAATG  
 GAGCCATGCACTTCCATGACTACAAGTCAGATGTACAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG  
 ATTACAGCGCAAGTACATGAAGCTTCGAGACTTCTCGGCTCATCTCAGGCATCCCTCTCCCTCCCCACCTG  
 ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGACTCTCTGTGGCATCCTCAGTGGGCACGTGCATGATCGGSGGCAGG  
 TGGGGGAGCCAATCAAGTCTGAAAGGCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGAACGCTCT  
 TCGGGTACATTTCTCTATGAGACCAGCATCACTCGTCTGGCATCCTCAGTGGGCACGTGCATGATCGGSGGCAGG  
 TGTTTGTGAACACAGTATCCATAGGATCTTGGACTACAAGACAACGAAGATGCTCTCCCTCATCCAGGTT  
 ACACCGTGTGAGGATCTTGGTGGAGAAATCGTGGGCAGTCAACTATGGGAGCAATATGATGACCAAGCCAAAG  
 GCTTAATTGGAAATCTTCTATGATGATTACCCCCGAAAACTCAGAAATCTATAGCTGGATATGAAGAAGA  
 GCTTCTTCCAGAGTCTCGGCTGGACAATGNGTTCCTCCCAAGAACCACTTACCTGCTTCTCTTGG  
 GTAGCTTGTCCATCAGCTTCCAGCCTTGTGACACCTTCTGAACTGGAGGGCTGGGAGAAAGGGGCTGTGATTC  
 TCAATGGCCAGAACTCTGAGCGTTACTGGAACTTTGGACCCAGAAAGACGCTTTACCTCCAGGCTCCTGGTTGA  
 GCAGCGGAATCAACAGGTATCTGTTTTGAGGAGACGATGGCGGCCCTGCATTACAGTTTACGGAAGACCCCC  
 ACCTGGGCGAAGCCAGTACATTAGTGAAGCGGTGGCACCCCTCTCTGCTGGTGGCAGTGGGAGACTGCCGCCCTC  
 CTCTTGACCTGAGGACCTGGTGGCTGCTGCCCAACCTCATCTGCAAAAGCATCTCTTAAGTAGCAACCTCAGG  
 ACTGGGGCTCAGACTTGGCCCTGTCTCAGCTCAAAACCTTAAGCTCGAGGAAAGGTGGGATGGCTTGGGCC  
 TGGCTTTGTGATGATGGCTTTCTACAGCCCTGCTCTTGTGCCGAGGCTGTGGGCTGTCTCTAGGGTGGGAGC  
 AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTTGACCGGACGTCAAGCCC  
 TGCAGCATCTGCTGGACTCAGGCGTCTCTTTGCTGGTTCTGGGAGGCTTGGCCACATCCCTCATGGGCCCT  
 TTATCCCGAAATCTGGGTGTGTACCATGTAGAGGGTGGGGAAGGGGTGTCTCACTGAGCTGACTTTGTT  
 CTTCTTCAACACTCTGAGCCTTCTTGGGATTTGGAAGGAACCTCGGCTGAGAAACATGTGACTTCCCTT  
 TCCCTTCCCATCTGCTGTTCCCAAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCTCAACCTGCTCTTCC  
 CAAGTTAGCAGGTGTCTCTGGTTTCACTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCATGTCTGCA  
 CATCCAGGAGGAGGACAGAAAGGCCAGCTCACTGTGAGTCTTGGCAGAAGCCATGGCCATGTCTGCAATCC  
 AGGAGGAGGACAGAAAGGCCAGCTCACTGTGAGTCTTGGCAGAAGCCATGGCCATGTCTGCAATCCAGGGA  
 GGAGGACAGAAAGGCCAGCTCACTGTGAGTCTTGGCAGAAGCCATGGCCATGTCTGCAATCCAGGAGGAGG  
 ACAGAAGGCCAGCTCAGTGCCCTCCCTCCACCCCCACGCCGACAGCAGGAGGAGGAGGAGGAGGAGGAGG  
 GAAGTGTGTCCAGTCCGATTTGAGCTGTCTTCTGGGGCCAGGCCAACACCTGGCTTGGGCTCACTGTCTGTA  
 GTTGCAGTAAAGCTATAACCTTGAATCACAA

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## **FIGURE 64**

MTTWSLRRRPARTLGLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW  
IFGGSIHYPFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDFSGNLDLEAFVLMA  
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLSRVVPLQ  
YKRGGPIIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKGLSKGIVQGVLAT  
INLQSTHELQLLTFTFLFNVQGTQPKVMMEYWTGWFDSWGPPHILDSSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP  
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLNVNGGNGQSFGYIILE  
TSITSSGILSGHVHDRGQVFVNTVSI GFLDYKTTKIAVPLIQGYTVLRLIVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXS L PETPTLPAPFLGSL SIS  
STPCDTFLKLEGWEGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

### **Signal sequence:**

amino acids 1-27

### **Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

### **N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586





## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDGRHDFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLCLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFS YMRHLA GLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVD FGPADNM TKIF  
TLLRKYPEHGPLVNSEYTGWLLDYWGQNHSTRSVSAVTKGLENMLKLGASVNM YMFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFM L YRTYMTHTIFEPTPFWVPN  
NGVHDRAYVMVDGVFQGVVERNM RD KLFTGKLGSKLDILVENMGR L SFGSNS SDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLEEDVPLQPQVQFLD  
KPILNSTSTLHRTHINLSADTLSASEPMELSGH

### **Signal sequence:**

amino acids 1-27

### **N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

### **Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

### **Tyrosine kinase phosphorylation site.**

amino acids 191-198

### **N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490



## FIGURE 68

MAYMLKLLISYISIIICVYGFCLYTLFWLFRIPLKEYSF EKVREESSFS DIPVKNDFAFL  
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTFEKL RQHISRNAQDKQELHLFMLS G  
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLC HCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLNS ENNMIGLES LRELRLHLKILHVKS NLTKVPSN  
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAE LELQNCELERIPHAIFSLSNLQELDLKS  
NNIRTIEEIIISFQHLKR LTKLWHNKIVTIPPSITHVKNLES LYFSNNKLES LPVAVFSLQ  
KLRCLDVSYNNISIMPIEIGLLQNLQHLHITGNKVD ILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLS QLTQLELKGNC LDR LPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

### **Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

### **Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

### **N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## FIGURE 69

CCCACGCGTCCGGCCCTTCTCTCTGGACTTTGCATTTCCTTTTCATTGACAACTGACTTTTTTTTATTTCT  
 TTTTTTCCATCTCTGGGGCAGCTTGGGACTCTAGGCGCCCTGGGAAGACATTTGTGTTTACACACATAAGGAT  
 CTGTGTTTGGGGGTTCTTCTTCTCCCTGACATTTGGCATGCTTAGTGTTGTGTGGGGAGGAGACCACTGTG  
 GCTCAGTGCTGTGCTTGCACTTATCTGCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCTTGT  
 ATCGCTGGTGGTATCTCTGGCGGCTTGTCTCTGTGATAGTTGTGTGCTTGTCTTTACTTCAAAAATACAAC  
 GCGCTAAAAGCTGCAAGGAACCTGAAGCTGTGGCTGTAAAAAATCAACAACCCAGACAGGTGTGGTGGGCGAAG  
 AACAGCGAGGCGCAAAACCATTTGCCACGGAGTCTTGTCTGCGCTGCAGTGCTGTGAAGGATATAGAAATGTGTGCC  
 AGTTTTGTATTCCTGCCACCTTGTGTGTGCACATAAATGAGGGCTCTGAGTTAGGAAGGCTCCCTTCTCAAA  
 GCAGAGCCTCGAAGACTTCAATGATGTCAATGAGGCCACCTGTTGTGATGTGCAGGCACAGAAGAAAGGCACAG  
 CTCCTCATCAGTTTCATGGAAAAATACTCAGTGCCCTGCTGGGAACCACTGCTGGAGATCCCTACAGAGAGCTTC  
 CACTGGGGCAACCCCTTCAGGAAGGAGTTGGGGAGAGAGAACCTCACTGTGGGGAATGCTGATAAACCACTCA  
 CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGGTGGCTGGAACTGACGTTTCCCTGGAGGTGCTCCAGAAA  
 GCTGATGTAACACAGAGCCTATAAAAAGCTGTGCGTCTTAAGGCTGCCAGCGCTTGGCAAAATGGAGCTTGTA  
 AGAAGGCTCATGCCATTGACCTCTTAATTTCTCTCTGTTTGGCGGAGCTGACAAATGGCGGAGGCTGAAGGCAAT  
 GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC  
 AGTGAGAACTGCACCTGGCAATAGAAAGACCAGAAAAACAAAGCATCAGAAATATCTTTTCTATGTCCAGCTT  
 GATCCAGATGGAAGCTGTGAAAGTGAACACATTAAGTCTTTGACGGAACCTCCAGCAATGGGCTCTGCTAGGG  
 CAAGTCTGCAGTAAAAACGACTATGTTCTCTGATTTGTAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT  
 GACTCAGCAAGAAATTCAAAGAACTGTTCTTGTCTTCTACTACTTCTCTCTCCTAACATCTCTATTCCAACTGT  
 GCGGTTACCTGGATACCTTGGAGGATCTTCCACAGCCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT  
 TGTGTGTGGCATAACAAGTGGAGAAAGATTACAAGATAAACTAAACTCAAAGAGATTTTCTAGAAATAGAC  
 AAACAGTGTCAAATTTGATTTCTTGCCCATCTATGATGGCCCCCTCCACCAACTCTGGCTGATTTGGACCAAGTCTGT  
 GGGCGTGTGACTCCCACTTTCGAATCTGTCATCAAATCTCTGACTGTGTGTTGTCTACAGATTTGCCAATGCA  
 TACCGGGGATTTTCTGCTCCTCAACCTCAATTTATGCAGAAACACTCAACCACTATCTTTAACTTGTCTCTTCT  
 GACAGATGAGAGTATTTATAAGCAATCTACCTAGAGGCTTTAACTCTAATGGGAATACTTGGAACTAAAA  
 GACCCAACTTCGACAGCAAAATATCAAAATGTTGTGGAAATTTCTGTCCCTCTTAATAGGATGTGGTACAATCAGA  
 AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACTTTTCTGCATCTCCAATCTTCAAGTGTGCACT  
 CGTCAGAAACCACTCCAGATTATTTGTGAAGTGTGAATGGACATAAATCTCAAGTGGAGATAATATACATAACA  
 GAAGATGATGTAATACAAAGTCAAAATGCACTGGGCAAAATATAACACCAAGCATGGCTCTTTTGAATCAATTC  
 TTTGAAAGAGTACTACTTGAATCACCATATTATGTGGATTGAAACCAAACTCTTTTGTTCAGTTAGTCTGCAC  
 ACCTCAGATCCAAATTTGTGTGTGTTCTTGATACCTGTAGAGCCTCTCCCACTCTGACTTTGCATCTCCAAC  
 TACGACCTAATCAAGATGGATGTAGTTCGAGATGAAACTGTAAAGTGTATCCCTATTTTGGACATATGGGAGA  
 TTCCAGTTTAATGCCCTTTAAATCTCTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAAGTTTGTATATGTGAT  
 AGCAGTGACCACCACTCTGCTGCAATCAAGGTTGTGTCTCCAGAGCAACAGAGACATTTCTCATATAAATGG  
 AAAACAGATTCATCATAGGACCAATTCGTCTGAAAAGGGATCGAAGTGCAGTGGCAATTCAGGATTTCCAGAT  
 GAAACATGTGCGGAAGAACTCCAAACCAAGCTTTCAACAGTGTGCATCTGTTTCTTCTCATGGTTCTAGCTCTG  
 AATGTGTGATCTGAGCGCAATCAGAGTGGGCTTTTGTAAATCAACGGGCGACACTCAAAATACAGAAAGCTG  
 CAGAACTATTAACCTAACAGGTCCAACCTAAGTGAGACATGTTTCTCCAGGATGCGAAAGGAAATGCTACCTCTG  
 GGCTACACATATTATGAATAAATGAGGAAGGCCCTGAAAGTGACACACAGGCTCGATGTAAAAAA

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## FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGCTG  
TGCTGCGCCCGCCCGCGTGCCTGCCACAGCGCCACCGCGCTTCGACCCACCTGGGGAGTCC  
CTGGACGCCCCGCCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG  
GGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTTGGCAAAAGGAAA  
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAAATATGAAGAT  
TTTGGACCACTATTACAGCAAAATTTTTTAATGCCAACCCAGTGGGCAGATATTTTTTCAGGC  
CTCTGGTGCCAAATACATTGTCTTAACTTCCAACATCATGAAGGCTTTACCTTGTGGGGGT  
CAGAATATTCTGGGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAAGTACCTCGCGTTTTGGACTGTACTATTCCTTTTTTGA  
ATGGTTTTATCCGCTCTTCTTGGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG  
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGAGGAGCACCCGATCAATACTGGAACAGCACAGGCTTCTTGGCCCTGGTT  
ATATAATGAAAGCCAGTTCCGGGCCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA  
TCTGTAAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA  
CATAAATGGGAAAACATGCATGACAAATAGACAACTGTCTTGGGGCTATAGGAGGGAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTTCATGTG  
GAGGAAATCTTTTGATGAATATTTGGGCCACACTAGATGGCACCATTCTGTAGTTTTTTGAG  
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAAACCTA  
TACCTGGCGATCCAGAAATGACACTGTACCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTCTCTTGGCCAT  
CCCAAAGCTATTCTGGGGGCCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG  
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCAATTTCATCAGATGC  
CGTGTAAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACTGGATAAGAAAATTAATTGGCAGTTTCAGCCCTTCCCTTTTTCCCACTA  
AATTTTCTTAAATTACCCATGTAAACATTTTAACTCTCCAGTGCACTTTGCCATTAAAGTC  
TCTTCACATTGATTGTGTTCCATGTGTGACTCAGAGGTGAGAATTTTTTTCACATTATAGTAG  
CAAGGAATTTGGTGGTATTATGGACCGAACTGAAAAATTTATGTTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGTCTAGTCAAT  
TTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAACATAGAGAAG  
GTACAGTAAAAATCTGTAATAATAATGGTGACCTGTATAGGGCACTTACCACGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAAATCTGTATGCTTAGGCTACACTACATTATATAAAAAAA  
GTTTTTCTTCTTCAATTATAAAATTAACATAAGGTGACTGTAACCTTACAAACGTTTTTAATT  
TTTAAACCTTTTTGGCTCTTTGTGATAAACACTTAGCTTAAACATAAACTCATTGTGCA  
ATGTA

## **FIGURE 72**

MRPQELPRLAFPLL LLLLLLLLPPPPCPAHSATRFDP TWSLDA RQLPAWFDQAKFGIFIHWG  
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLT SKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW  
FHP LFLEDESSSFHKRQFPVSKTLP ELYELVN NYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGT VVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGNNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDT VTPDVWYTSKPKEKLVYAI FLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKKGWALALTNVI

### **Signal sequence:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

### **Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

### **Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

### **N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

### **Leucine zipper pattern.**

amino acids 410-432

### **Alpha-L-fucosidase putative active site.**

amino acids 283-295



## FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT  
TCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGCCATC  
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCAGTCTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT  
TTCCATCCAGGTGTCTATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGC  
AGCTGAATTTCCAGTAGAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGAGCTATGGCTGGGTTGGAGA  
TGGATTTCGTGGTCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTG  
TCCTGATTGGGAAGGTTCCAGTGAGCCGACAGTTTGAGCCTATTGTTACAACCTCATCTGAT  
ACTTGGACTAACTCGTGCAATCCAGAAATTATCACCACCAAGATCCCATATTCAACACTCA  
AACTGCAACACAAACACAGAATTTATTGTGAGTGACAGTACCTACTCGTGGCATCCCCTT  
ACTCTACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGG  
AGAAAAAATTGATTTGTGTACAGAAAGTTTATGGAACCTAGCACCATGTCTACAGAAAC  
TGAACCATTTGTTGAAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTC  
CCACGGCTCTGCTAGTGTCTGCTCTCTCTCTTTGGTGTGTCAGCTGGTCTTGGATTTTGC  
TATGTCAAAAGGATGTGAAGGCTTCCCTTTTACAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAGTAGTAAAGGAGGAGAAGGCCAATGATGCAACCCCTAATGAGGAATCAAAGA  
AAACTGATAAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCGCTGAA  
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTTTCATGCTCC  
TTACCTTGCCCGAGCTGGGGAATCAAAGGGCCAAAGAACCAAGAAGAAAGTCCACCTT  
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGC  
CCTTCTCTTATTGTAAACCTGTCTGGATCCTATCCTACCTCCAAAGCTTCCCACGGCC  
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAA  
GGACCTAAAAATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCTGGCTGTCTGAGGCTAGG  
TGGGTTGAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGAC  
CCTTCTCTCAGCTCTGAAAGAGAAACACGTATCCCACTGACATGTCTTCTGAGCCCGGTA  
AGAGCAAAAGAAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGTAAGCTAAAAATAAGAAATAGAACAAGGCTGAGGATACGACAGTACCT  
GTCAGCAGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGTAACACATTGAGTTGGA  
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT  
AGGAAATATACTTTTACAAGTAACAAAAATAAACTCTTATAAATTTCTATTTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTTAAAAAGTAATAAAATTA  
ACAAACATTGTGTAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCTCAAAAAATTGCACATAGTAGAAGCTATCTGGGAAGCTATTTTTCAT  
GTTTGTATTTCTAGCTTATCTACTTCCAACTAATTTTATTTTTGTCTGAGACTAATCTT  
ATTCAATTTCTCTAATATGGCAACCATTAACCTTAATTTATTATTACATACCTAAGAG  
TACATTTGTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAAACAAATGTATCATA  
GCCCTCCTTTTCCCAACAAGAAGGAGTCTGAGAGATGCAGAAATATTTGTGACAAAAATAA  
AGCATTTAGAAACTT

## FIGURE 74

MARCFSLVLLLTISIWTRLLVQGSSLRAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACR  
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQF  
AAYCYNSSDTWTNSCIPEIIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAPKNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFFFTNKNQQKEMIE TKVVKEEKANDSNPNEESKKT DKNPEESKSP  
SKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGATTTCGGTGCCGCGACTTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCTTCTACTCTGTGAGGAA  
ACTGCCGCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT  
TCTTTTCTCCGCTTGGATATTGCGATGGGCCTACTTTACATCACACTCTGCATAGTGTTC  
TGATGACGTGCAAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAAGTAGAACGGGACAAGAGGGTCACCTTGGATTGTGGAGTTCCTTGGCAA  
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAACT  
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC  
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG  
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACGACGGGCCAAGAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACACAGTGTGAGA  
TGGGGAAAACAAGAAGGATAAA**TA**AGATCCTCACTTTGGCAGTGCTTCTCTCTGTCAATT  
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNNATNNATGTTTTCCCTTTGG  
CTGNGACTGGNTGGGCGCATGCGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG  
GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGTGTTCCTGAGGCAAGAAAGAGATC  
TCATAGGACGAGGGGGAAATGGTTTCCCTCAAGCTTGGGTGAGTGTGTTAACTGCTTATC  
AGCTATTACAGACATCTCCATGGTTTCTCCATGAACTCTGTGGTTTCATCATTCTCTTAG  
TTGACCTGCACAGCTTGTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAA  
CGCTAAGAATTTTCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC  
TTCATTAAAGTATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAG  
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTTCAC  
TAACCTCTGACATACTCCCCACCCAGTTGATGGCTTCCGTAATAAAAAGATTGGGATT  
TCCTTTTG

## **FIGURE 76**

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGHNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYN  
TGLNFGKVDVGRYTDVSTRYKVSTSP LTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

### **Signal sequence:**

amino acids 1-48

### **Transmembrane domain:**

amino acids 111-125

### **N-glycosylation site.**

amino acids 165-169, 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

### **N-myristoylation site.**

amino acids 188-194, 225-231

### **Myb DNA-binding domain repeat signature 1.**

amino acids 244-253



## FIGURE 78

MGLLLLVLPLLLPGSYGLPFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRIRYEPALVSPRRVRVKWWKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRRLLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

### **Signal sequence:**

amino acids 1-17

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

### **Tyrosine kinase phosphorylation site.**

amino acids 137-145

### **N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC  
TTCTGTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAAGCGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACCGGAA  
CTTCCAGTACGACCATGAGGCTTTCTTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGAC  
GGCGACGGCTGGGTGTCTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA  
CATACGGGACTCGGTGAGCGCGGCCCTGGGACACGTACGACACCGGACCGCGACGGGCGTGTGG  
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGTGAAGAATTTTCATGAC  
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGCGGTTTCCGGGTGGC  
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCTGACCCCCGAGG  
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA  
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGACTCTGAACAAGG  
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACCAGCCC  
CTGGTGAAGCCAACCACTGCTGCACGAGAGCGACACGACAAGGATGGCGGCTGAGCAA  
AGCGGAAATCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACCACGATGAGCTGTGAGCACCCGCGACCTGCCACAGCCTCAGAGGCCCG  
CACAATGACCGGAGGAGGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGAGGAG  
GCAGATGCAGTCCCAGGCATCTCTGCCCTGGGCTCTCAGGGACCCCTGGGTGGCTTC  
TGTCCCTGTACACCCCCAACCCAGGGAGGGGCTGTCTAGTCCCAGAGGATAAGCAATAC  
CTATTCTGACTGAGTCTCCCAGCCCAGACCCAGGGACCCCTTGGCCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCT  
GGCCCCAGCCCTCTCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA  
AAGCCAGCGCCGGGACCTTGAAAAA  
AAA  
AAAAAAAAAAAAAAAAA

090395.07101

**0710**

Signal sequence:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330



## FIGURE 81

GGGGCCTTGCCCTTCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
GGGGCGGGCGCGGGTGCCGAGGGATCCCTGACGCCCTCTGTCCCCTGTTTCTTTGTGCGCTCCAG  
CCTGTCTGTGCTCGTTTGGCGCCCCGCCCTCCCGCGGTGCGGGGTGGACACCGATCCTG  
GGCTTCGCTCGATTTCGCCCGGAGGCGCCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCTGTGTCCTCTCTCCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGGCGGGCTCT  
GAGGAGGTGACGCGCGGGGCCCTCCCGCACCTGGCCTTGCCCGCATTTCTCCCTCTCTCCAG  
GTGTGAGCAGCCTATCAGTCACCAATGTCCGCAGCCTGGATCCCGGCTCTCGGCCCTCGTGTG  
TGTCTGCTGCTGCTGCCGGGGCCCCGGGGCAGCGAGGGAGCCGCTCCCATTGTCTATCACATG  
TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCCTCGCCAGGGGGCTGCC  
CTCTTGAGGAATTTCTCTGTGATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAACTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAAATGCTTTCTAGAT  
GGTCTGCTCTTTTACAGTAACAAAGGCCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCCAAACAGGTAAACGACTAAAGAAAAACCCCGAGAAGAAAACTGG  
CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC  
GCCGATTTAATTTACAGAAGAAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA  
GAAGGACCACATGTGGGCTTGTTCAGGCCAGTGAACATCCCAAAATAGAAATTTACTTGA  
AAACTTTACATCAGCCAAAGATGTTTTGTTTGGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA  
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTTCTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA  
AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGT  
CGGAATAATGGCTTCTTCTTACCACATGCCCAACTGGTTTGGCACCAAAAAACGTAA  
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT  
CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCTC  
ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAATCTCGGACATTGGTGCCAAGAT  
AGCTGCTGTACAGTTTACTTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACA  
AAGAGAATGTCCTAGCTGTCTATCAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT  
GATGCCATTTCCCTTCACTGTTAGAAAATGTGTTTGGCCCTATAAGGGGAGAGCCCCAACAGAA  
CTTCCTAGTAATTTGTACAGATGGGCAGTCTCATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTTCTCTGTGGTGTGGCTTGGGCACCTCTGGATGACCTG  
AAAGATATGGCTTTAAACCGAAGGAGTCTCACGCTTTCTTCAAGAGAGTTTCAAGGATT  
AGAACCAATTGTTTCTGATGTCTATCAGAGGCATTTGTAGAGATTTCTTAGAATCCAGCAAT  
AATGGTAAACATTTTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTTGTATT  
CTCATAAATCTGAAATGCTTTAGCATACTAGAATCAGATACAAAACATTAAAGTATGTCAAC  
AGCCATTTAGGCAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT  
ACTTTGTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAACCTTAAGAGTTCTAACCATGCTACTAAATGTACAGATATGCAAA  
TTCCATAGCTCAATAAAGAATCTGATACTTAGACCAAAAAAAAAA

## **FIGURE 82**

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEFVSVY  
GNIVYASVSSICGAAVHRGVISNSGGFVVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSPNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDLFAIKEVGFRGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCHEQMMSCKTCYNSVNIAFLI  
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTFESFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHADAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

### **Signal sequence:**

amino acids 1-24

### **N-glycosylation site.**

amino acids 100-104, 221-225

### **Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

### **N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

### **Amidation site.**

amino acids 145-149

## FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCGCCACCGCGCGCTCCCGCATCTGCACCCGAGCCC  
GGCGGCCTCCCGCGGGAGCGAGCAGATCCAGTCCGCGCCCGCAGCGCAACTCGGTCCAGTCG  
GGGCGCGGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCTGTGTGTGCTGC  
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC  
AAGCCCCGGCCCGGTCTCAGCTACCCCGCAGGAGGAGGCCACCTCAATGAGATGTTCCGCGA  
GGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAAGAGATGGAGG  
CAGAAGAAGCTGTCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTAT  
CACAATGAGACCAACACAGACACGAAGGTTGGAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACACAGACTGGACAAAATGGTCTTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGCAGAAGGAGCCACAGTGCATCATCGACGAGGACTGTGGGCCCAGC  
ATGTACTGCCAGTTTGGCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACAAAA  
TGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACACCCAGAGGGACTGCCAGCCGGGGCTG  
TGCTGTGCCCTCCAGAGAGGCTGTCTGTTCCTGTGTGCACACCCCTGCCCGTGAGGGCGA  
GCTTTGCCATGACCCCGCCAGCGGCTTCTGGAACTCATCACTGGGAGCTAGAGCCTGATG  
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCGACCTCTGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTATGGAGGAGGTGCGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCGGCTGCCGCGCT  
GCACCTGTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA  
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCTTACA  
TCTTCTTCCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTCCAGC  
TCCCCCAGGCTGTTCTCCAGGCTTCAAGTCTGGTGCTTGGGAGAGTCAAGCAGGGTTAAAC  
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAG  
ACAGCGCTTGTCTACATAGGCTTTGATAATTGTTGAGGGGAGGAGATGGAAACAATGTGG  
AGTCTCCCTCTGATTGGTTTTGGGAAATGTGGAGAAGAGTGCCTGTCTTGCAAAACATCAA  
CCTGGCAAAAATGCAACAAATGAATTTCCACGCAGTCTTCCATGGGCATAGGTAAGCTG  
TGCCCTCAGCTGTGTCAGATGAAATGTTCTGTTTCAACCTGCATTACATGTGTTTATTTCATCC  
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC  
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCAATTGTTCTCCTCGTCCATCAGGGATCTCAGAG  
GCTCAGAGAGCTCAAGCTGCTTGCCCAAGTCACACAGCTAGTAGAAGACCCAGCAGTTTTCAT  
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACAGGCCCTTGGTGCCACAA  
AAGTGCTCCCCAAAGGAAGGAGAATGGGATTTTTCTTGGAGCATGCACATCTGGAATTAAG  
GTCAAACATAATTTCCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC  
AGTGTGGGCGAGCGCTCCTTCTAATGAAGACAATGATATGACACTGTCCCTCTTTGGCAGT  
TGCATTAGTAACTTTGAAGGTATATGACTGAGCGTAGCATACAGGTTAACTCGAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC  
TGAAGACAATTATCAACACCTGGAGAAAAATCAACCGAGCAGGGCTGTGTGAAACATGGTT  
GTAATATGGCAGTCGCAACTGAACTCTACGCCACTCCAACAAATGATGTTTTAGGTTGTCA  
TGGACTGTTGGCCACCATGTATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGTGTA  
TAAGCATGCTTTCTTTGAGTTTTAAATATGTATAAACATAAGTTGCATTTAGAAATCAAGC  
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEEAAKASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHBCIIDEDCGPSMYCQFASFQYTCQPCRQGRMLCTRDSECCG  
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEIILLPREVPDEYEV  
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEET

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144

09039256

AAA



## FIGURE 87

GCAAGCCAAAGGCGCTGTTTGAAGAAGTGTCCGGACCCATGTGGAGGAGGGGGACATTGTGTATCCGCCCT  
CTACATGCGGGCAGACCATTATCAAGGTGATCAAGTTTCATCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTTCGACGTGGAGCTGACCGTGGACATTTAGAGCCTGACGGGTACCGCACCTACCGCTGTGCCACCC  
CCTGGCCACACTCTTCAAGATCCTGGCGTCTTCTACATCAGCCTAGTCATCTTCTACCGGCTCATCTGCATGTA  
CACATCTGTGTGGATGCTACCGGCTCCCTCAAGAAGTATCTGTTTGTAGTCGATCTCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGACGCTCAAGAACGACCTTCGCCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA  
GCGCTTCGCCCTCTTCTCTGCGGAGTGTGAGTGAAGAACAAGCTGCGGCAGCTGAACTCTCAACAACGAGTGGAGCGCT  
GGACAAGCTTCGGGACGCGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACTCTGTTTCATGCTCAGTGGCAT  
CCCTGACATCTGTGTTTGAACCTGTGGTGGAGTCTCTCAAGCTGGAGCTGATCCCGCAGGTGACCCGCTGCCGC  
CAGCATCTTGCCAGCTCACGGGCTCAAGGAGCTGTGGCTCTACACACAGCGGCCAAGATTGAAGGCGCTGTGGCT  
GGCTCTCTGCGCGAGAACTCGCGGCGCTGCACATCAAGTTTCAACGACATCAAGGAGATCCCGCTGTGGATCTA  
TAGCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAAACCGCTACATCGTCATCGA  
CGGCTGCGGGAGCTCAAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGTCTAC  
AGATGTGGGCTGCACCTGCAGAACTGTCCATCAACAATGAGGGCAACAAAGCTCATCTGCTCTCAACAGCCTCAA  
GAAGATGGCGAACTGACTGAGCTGGAGCTGATCCGCTGCGACCTGCGGCGCATCCCCCACTCCATCTTTCAGCCT  
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT  
GCACCGCTCACCTGCCTTAAGCTGTGGTCAAAACCATGCGCTACATCCCATCCAGATCGGCAACCTCAACAA  
CCTGGAGCGCTCTACCTGAACCGCAACAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCGCCCAAGCTGCG  
CTACCTTGGACCTCAGGCCAACCAACCTGACCTTCTCTCTGCGGAGTGGGCTCTCTGAGAACTCCAGAACT  
AGGCCACTCAGCGCAACCGATCGAGCGCTCTCTCCGGAGCTCTTCCAGTCCCGGAAGCTGCGGGCTGCACCT  
TGGCAACAAAGCTGCTGCTCACTGCTGCTCCCTCAGGCTGGGCGAGCTGACCAACTCTGAGCAGATCAGCTCGGGG  
CAACCGGCTGGAGTGCCTGCCTGTGGAGCTGGGCGAGTGCCTCAAGCGCAGCGCTTGTGTGTGGAGGA  
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCGTGAAGCGAG  
GCGGCGCAGCAGCAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCGCGAGGGGCGAGGCTTAGCTTCTCCAG  
AATCTCCGAGCAGCGCAGGACAGCTCTCGCGCTGGGCGAGGAGCTGGGGCGGCTGTGTAGTCAAGCCAGAGCGAGA  
GGACAGTATCTGTGGGGCTGGGCCCTTTCTCCCTCTGAGACTCAGCTTCCCGAGGCGAGTCTGTGTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCTCTCTGGAGGCCAGCTCTGCCCCAGGGGGCTGAG  
CTGCCACAGAGGCTCTGGGACCTCCTTCTTAGTTCTTGGTATTTATTTTCTCCATCTCCCACTCTTTCATCC  
AGATAACTTATACATTCCCAAGAAAGTTTCAGCCAGATGGAAGGTGTTTCAGGGAAGGTGGGCTGCCTTTCTCCC  
TTGTCTTATTTAGCGATGCGCGGGGCTTTAAACCCACCTGGACTCTCAGCAGAGTGTCCGGGGCGAAGCAG  
CCATGGAGCGGTCAACCCAGCAGTGCCTGGCTGGGCTCTGCGTGTGCGTCCACGGGAGAGCAGGCTCAGCTGGA  
AAGGCCAGGCGCTGGAGCTTGCTCTTCAAGTTTGTGGCAGTTTAGTTTCTTGTGTTTTTTTAAATCAAA  
AAACAATTTTTTTTAAAAAAAGCTTTGAAAAATGGATGTTTGGGTATTAAGAAAGAAAAAACTTAAAAAA  
AAAAGACACTAACGGCCAGTGAAGTTGGAGTCTCAGGCGAGGCTGGCAGTTTCCCTTGAGCAAGCAGCCAGCAGT  
TGAAGTGTGTTTCTCTTCTCTGGGCGCAGGCTGACGGTGTCTTCCGGATCTGTGTGACCTTGGTCCAGGAGTT  
CTATTCTCTGGGGAGGGAGTTTTTTTGTGTTTTTGGGTTTTTTTGGTGTCTGTGTTTTCTTCTCTCC  
ATGTGCTTGGCAGGCACTCATTTCTGTGGCTGTGCGGCGAGGGAAATGTTCTGTGAGCTGCCAAGGAGGGAGGAG  
ACTCGGGTTGGCTAATCCCGGATGAACGCTGCTCCATTGCACTTCCCTCTCTGCTGCGCTCGCTGCTTCCA  
CGCACAGTGTAAAGGAGCCAGGAGGCCAATTCGCCAGACTTTGTTTCCCACTCTCTGCGCATGGGTGTGT  
CCAGTGCCACCGCTGCGCTCGCTGCTTCCATCAGCCCTGTGCGCACTGGTCTTCATGAAGAGCAGACATTA  
GAGGCTGTGTGGGAATGGGAGGTGCGCCCTGGGAGGGCAGGCGTGTGTTTCCAAGCCGCTTCCGCTCCCTGGCGC  
CTGGAGTGCACAGGCCACTGCGCACTGTGGCTGGAGGCCAACCTGTCTTAGATCACTCGGGTCCCACTCT  
AGAAGGGTCCCCGCTTAGATCAATCAGGTGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT  
CCATCGCTCTGCTGCTCATTTGTGTTTTCTGCGTGTGCTATTGGATATGCTCAGAAATAATGCACATAG  
CCTCTGACAACCATGAAGCAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAAATAA  
ATCTATAACAGAAAAA

090333.071401

## **FIGURE 88**

MRQTIKVIKFIILICYTVYYVHNKFDVDCTVDIESLTGYRTYRCAHPLATLTKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHLMFSLGIPDTVFDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLLELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQ  
HLHRLTCLKLWYNHIAIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRLALHLGNNVLQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

### **Transmembrane domain:**

amino acids 51-75 (type II)

### **N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

### **Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

### **N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447





## **FIGURE 90**

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNGLYRE  
ATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELEAGINVTYNGQLDL  
IVDTMGQEAWRKCLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

### **Signal sequence:**

amino acids 1-25

### **N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

### **N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366



## **FIGURE 92**

MGARGALLLALLLARAGLRKPESQEAAPLSGPCRRVITSRIVGGEDAELGRWPWQGSRLRW  
DSHVCVSVLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWSVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

### **Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

### **N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

### **Amidation site.**

amino acids 33-37

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

### **Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

# FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT  
 CTTTGCCCTCATCCTCTCTGGCAAAATGCAGTTACAGCCCGGAGCCCGACAGCGGAGGACGC  
 TGCCCCAGGCTGGGTGTCCCTGGGCCGTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTTT  
 GCCCTGAGACAGCAGAAATGTGGAAGACTCTCGGAGCTGGTGCAGGCTGTGTCCGATCCAG  
 CTCTCCTCAATACGGAATAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC  
 CACTGACCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCAGAAAGTGCCATTCT  
 GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
 TGGGGCTGAGTTTCATCATATGTGGGAGGACCTACGGAACCCTGTTGTGAAGGTCCCCAC  
 ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT  
 TTTCCCCAACATCATCCCTGAGGCAACGCTCCTGAGCCGCAAGGTGACAGGGACTGTAGGCGCT  
 GCATCTGGGGTAACCCCTCTGTGATCCGTAAGCGATACAACCTTGACCTACAAGACGTGG  
 GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTTGAGGACAGTATTTCCATGAC  
 TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTCACATCAGGCATCAGTAGC  
 CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGAGTTGAGGCCAGTCTAGATGTGCACT  
 ACCTGATGAGTGCTGGTGCCAAATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG  
 GGACAGGAGCCCTTCTGCACTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
 GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA  
 AACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCTCAGGTGACAGT  
 GGGGCCGGGTGTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG  
 CCCCTATGTCACCACAGTGGGAGGCACATCTTCCAGGAACCTTTCCTCATCAAAATGAAA  
 TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCCAAGCCCTTCATACCAGGAG  
 GAAGCTGTAACGAAGTTCCCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC  
 CAGTGGCCGTGCCCTACCCAGATGTGGCTGCACTTTCTGATGGCTACTGGGTGGTCAAGCA  
 GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCCTTACTCTGCTTGTGGGGGGTCCCTA  
 TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCTCTTGGCTTTCTCAACCCAG  
 GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCTGTCT  
 TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGTCTGGTCTGGCTGGGATCCTGTAAACAGGC  
 TGGGGAACACCAACTTCCAGCTTTGCTGAAGACTCTACTAACCCCTGACCTTTCTCTATC  
 AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTGAGTCCCTTATTTCTGCCCTGTG  
 GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA  
 TGCTGTGAGCTTTGACTTGAATCCCAACCTTACCATGCTCCATCATACTCAGGTCTCCCTACT  
 CCTGCTTAGATTTCTCAATAAGATGCTGTAACTAGCATTTTTTGAATGCCTCTCCCTCCGC  
 ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA  
 TTTCACTTGATATTCATTTCCCAATTCAGTGAAGGAGACCTCTACTGTACCGTTTACTCT  
 TTCTACCTGACATCCAGAAACAATGGCCTCCAGTGCACTTCTCAATCTTTGCTTTATG  
 GCCTTTCCATCATAGTTGCCCACTCCCTCTCTTACTTAGCTTTCAGGTCTTAACTTCTCTG  
 ACTACTCTTGTCTTCTCTCTCATCAATTTCTGCTTCTTATGGAATGCTGACCTTCAATTG  
 TCCATTTGTAGATTTTGTCTTCTCAGTTTACTCATTTGCCCTGGAAACAATCACTGACA  
 TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCAATAATGATTGATACCTCAAA  
 TGTA AAAA

03603655.071303





## **FIGURE 96**

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG  
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPFAKQLPGGRIHFSGYDNDRPGNLVYRFGCDVKDETYDLLYQQCD  
AQPAGASGSGVYVRMWRQQQKWERKIIGIFSGHQVDMNGSPQDFNVAVRITPLKYAQICYW  
IKGNYLDCREG

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 93-97, 207-211

### **Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

### **Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

### **N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

### **Serine proteases, trypsin family, histidine active site.**

amino acids 171-177



## FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGTGGTTT  
CTGGAGCGCCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAAATGGGACCCACCCTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC  
ACTGCTGCCCACTGTTTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGGAACCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCTGTGTATTCTTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCTTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCCATATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCC  
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA  
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG  
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCGCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCGCCCCCAC  
GACTTCCGGCCCCCGCCCCGGCCCCAGCGCTTTGTGTATATAAATGTTAATGATTTTAT  
AGGTATTTGTAACCTGCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTTATT  
CTCCAAAAAAAAAA

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
MVVSGAPPALGGGCLGTFTSLLLLLASTAILNAAIRIPVPPACGKPPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLTTSRWVITAAHCFKDNLNKPYLFVLLGAWQLGNPGSRSSQKVGVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWSIQDG  
VPLPHPQTLQKLKVP IIDSEVCSHLYWRGAGQGPIEDMLCAGYLEGERDACLGDSGGPLMC  
QVDGAWLLAGIISWEGECAERNRPGVYISLSAHRSWVEKIVQGVLGRAGGGGALRAPSQG  
SGAAARS

### **Signal sequence:**

amino acids 1-32

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879



## **FIGURE 100**

MHGSCSFLMLLLPLLLLLVATTGPGVGTALDEEKRLMVELHNLRYAQVSPASDMLHMRWDEE  
LAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTVVWAKTERIGCGSHFCEKLGVEETNIELLVNYEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTTPSSSLATGIPAFVLTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTTEVPVPSILAAHSLPSLDEEPPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSIDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSSLPGAEGPDKPSV  
SGLNSGPGHVWGPLLGLLLLLPLVLGIF

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

### **Glycosaminoglycan attachment site.**

amino acids 439-443

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

### **N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

### **Amidation site.**

amino acids 82-86, 172-176

### **Peroxidases proximal heme-ligand signature.**

amino acids 287-298

### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

# FIGURE 101

GTAACTGAAGTCAGGCTTTTCATTGGGAAGCCCCCTCAACAGAAATTCGGTCATTCTCCAAGTTAT**ATG**CTGGACGT  
 ACTTCTGTGTTCTCCCTCTGCTTGTCTTTTTCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTTTAT  
 CAAGGCAGATTCCATGAGCCACCTTCAAGGCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCC  
 AAATCTGGGACAGCTCTCGGCAAAATTATACACTTCTCTCTTGGCTGGAACAGGATTGTGAAATACCTCCCTGA  
 ACATCTGAAGAGTTCTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAAACGTGCAT  
 TCCAGCCCTACAGCTCAAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACTCCGGGTATTTTGACAA  
 TTTGGCCACAACACTCTCTTGTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCCAAGATGTTTAAACT  
 GCCCAACTCGACAACTCTCGAATTGAACCGGAACAGATTAAAAATGTAGATGACATGACATTCCAAAGGCTTGG  
 TGCTCTGAAGTCTCTGAAATGCAAGAATAAGAGTAACGAAACTTATGGATGCGAGCTTTTGGGGCTGAGCAA  
 CATGGAATTTTTCAGCTGGACCAATAACAACCTTAACAGAGATTACCAAAAGGCTGGCTTTTACGGCTTTGCTGATGCT  
 GCAGGAACCTCATCTTCAGCCAAAATGGCCATCAACAGGATCAGCCCTGAGCTCTGGAGTGTCTGCCAAGACTCAG  
 TGAGCTGGACCTAACTTTCAATCACTTATCAAGSTTAGATGATTCAAGCTTCTTGGCCTAAGCTTACTAAATAC  
 ACTGCACATTGGGAACAACAGAGTCAGCTACATGTCTGATTGTGCTTCCGGGGCTTCCAGTTTAAAGACTTT  
 GGAATCTGAAGAACATGAAATTTCTCGGACATTTGAAGACATGAATGGTCTTTCTCTGGGCTTGACAAACTGAG  
 GCGACTGATACTCTCAAGAAATCGGATCCGTTCTATTACTAAAAGGCCCTTCACTGGTTTGGATGCATTTGGAGCA  
 TCTAGACCTGAGTGACAAACCAATCATGTCTTTACAAGGCAATGCATTTTCCAAATGAAGAAATCGCAACAAT  
 GCATTTAAATACATCAAGCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCGGAAAACAACCTT  
 TCAGAGCTTTGTAATGCCAGTTGTGCCCATCTCAGCTGTCTAAAGGAAGAGCATTTTGTCTGTATGCCCGA  
 TGGCTTTGTGTGTGATGTTTCCCAACCCAGATCACGGTTCCAGCAGAAACACAGCTGGGCAATAAAGGTTT  
 CAATTTGAGTTTCACTGTCTCAGCTGCCAGCAGCTGATTCCCAATGACTTTTGTCTGGAAAGCAACAATGA  
 ACTACTCGATGATGCTGAAATGGAAAATTTATGCACACTCTCCGGGCCCAAGGTTGGCAGGTTGATGGAGTATACCC  
 CATCTTCCGCTGCGGAGTGGAAATTTGCGAGTGAGGGGAAATATCAGTGTGTCAATCTCCAATCACTTTGGTTT  
 ATCTACTCTGTCAAGAGCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCATGGATGCATCTCACAT  
 CCGAGCTGGGGCTTGCACTGCAAGCTTGGAGTGTGCTGTGTGGGGCACCAGCGCCCATGAGCTGGCAGAAAGGA  
 TGGGGGCACAGACTTCCAGCTGCACGGGAGAGACGCATGATGTGATGCCCGAGGATGACGTGTTCTTTATCGT  
 GGATGGAAGATGAGGACATTTGGGTATACAGCTGCACAGCTCAGAAACAGTGACGGAAGTTTTCAGCAAAATG  
 AACTCTGACTGTCTAGAAACACCAATCATTTTGGCGGCACTGTGGACCGAATGTAACCAAGGGAGAAACAGC  
 CGTCTCAGTGCATCTGTGGAGGAAGCCCTCCCTCAAACCTGAACCTGACACCAAGATGATAGGCCCATTTGGTGGT  
 AACCGAGAGGCACTTTTTCGACAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCTGATGATGCTGGGAA  
 ATACACATGTGAGATGCTAACAACCTTGGCACTGAGAGAGGAAACGTCGCCCTCAGTGTGATCCTCCACTCAAC  
 CTGCGACTCCCTCAGATGACAGCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGATCATAGC  
 CGTGGTTTGTGTGGTGGGCACTGCTGCTGTGGGTGCTCATATATACCAACAAGGCGGAGGAATGAAGA  
 TGTGAGCATTACCAACACAGATGAGACCACTTGCAGCAGATATTCTAGTTATTGTTCATCTCAGGGAACGTT  
 AGCTGACAGGCGAGGATGGGTACGTGCTTTCAGAAAGTGAAGGCCACCACTTGTGTCACATCTCAGTGTGGT  
 ATTTTCTTACCAACACATGACAGTAGTGGGACCTGCCATATTGACAAATAGCAGTGAAGTGTGATGTGGAGCTGC  
 TCCCTTTGAAACATATCATACAGGTTGTCAGTCTGACCACGAACAGTTTAAATGGACCACTATGAGCCAGTTA  
 CATAAAGAAAAGGAGTGCTACCAATGTTCTCATCTCAGAAGAACTCCTGGAACCGAGCTTCAGATAATATAT  
 GTGGCTTTCATGTGAGGAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAAATGAAAATCTGTG  
 TCTAAACAAGTCCCTTTAGATTTTAGTGTCAAAATCCAGAGCCAGCGTGGTTGCTCAGATAATTCTTTATGGG  
 TACCTTTGGAAAAGCTCTCAGGAGACCTCACTAGATGCTTATTCAAGCTTTGGACAGCCATCAGATTGTGACGG  
 AAGAGCTTTTATTGAAAGCTCATTTCTCCCAAGCTTGGACTTGGGTGAGGAAGATGGGAGAAAGAGGAC  
 AGATTTTCAGGAAGAAATACATATTGTACCTTTAAACAGACTTTAGAAAATCAGGACTCCAAATTTTCAGTC  
 TTATGACTGTGACACAT**TAG**CTGAATGAGACCAAGGAAAGCTTAACTACTACTCTCAAGTGAACCTTTTATTTA  
 AAAGAGAGAGATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAATGCCTTATTTTATACAGAT  
 GACCAAAATTTACAAAAGTTATGAAAATTTTATATCTGGAATGAGTCTCATATAAGATTAATTTTAAACTA  
 TTTTAACTTTTGTGTTTATGCAAAAAGATATCTTACGTAAATTAATGATATAAATCATGATTTTATGTATTT  
 TTATAATGGCAGATTTCTTTTATGGAATAGTTACTAAAGACTTTTAAATGACTTCCCTGTGACCATTTT  
 TTAATAGAAGTTACTTCAATATATTTTGCACATTAATTTTAAATAAGTGTCAATTTGAA

090325.07101

## FIGURE 102

MVDVLLLFSLCLLPHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSA  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPAQLKYLNLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPLQHLLELNRRNIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMDGAFWGLSNMEIILQLDHNNLTETIKGWLYGLMLQELHLNSQAINRISPDWE  
FCQKLSLELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSSLKTLDLKNNE  
ISWTIEDMNGAFSGLDKLRRLILQGNRIRISITKKAFTGLDALEHLDSLDAIMSLQGNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWLPLQWVAENNFQSFVNASCAPQLLKGSRIFAVSPDGFVCD  
DFPKPIQITVQPETQSAIKGSNLSEFCSAASSSDSPMTFAWKDNELLHDAEMENYAHRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVMNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPAQIAWQKGGTDFPAARERRMHVMPEDDVFFIIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTER  
HFFAAGNQLLIIVDSVSDAGKYTCMSNTLGTGRGNVRLSVIPTPTCDSFQMTAPSLDDDG  
WATVGVVVIIVAVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLDLAD  
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSADVEAATDLFLCPFLGSTGP  
MYLKGNVYGSDDPFETYHTGCSGDPDRTVLMDHYEPSYIKKKCEYPCSHPSSESCERSFSNISW  
PSHVRKLLNTSYSHNEGFGPMKNLCLNKSSLDFSANPEPASVASSNSFMGTFTFGKALRRPHLDA  
YSSFGQPSDCQPPAFYLKAHSSPDLDGSEEDGKERTDFQEEHNHICTFKQTLNRYRTPNFQS  
YDLDT

### Signal sequence:

amino acids 1-19

### Transmembrane domain:

amino acids 746-765

### N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### Glycosaminoglycan attachment site.

amino acids 826-830

### Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### Tyrosine kinase phosphorylation site.

amino acids 607-615

### N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879



## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGI STNTRLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNPNIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDIL  
WLSWWIKDMAPSNTACCARCNTPPNKGRI GELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
LKCRATSLTSVSWITPNGTVMTHGAYKVRIVLSDGT LNFTNVTVQDTGMYTCMVNSVGN  
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTFPVVDWETTNVTTSLTPQ  
STRSTEKTF TPIPTDINSIGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
HHAPT RTVEI INVDDEITGDTPMESHLMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

### **Signal sequence:**

amino acids 1-44

### **Transmembrane domain:**

amino acids 523-543

### **N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

### **Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

### **N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537



# FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCCTTTTCGGGTTTCCCTCCTGCTGTTTGGGGGCA  
TGAAGGAGCTTTCGCCCGCGGAGCTAAAGAAAGGAATTAACCGGGCAGCGCGGAGGAGGAGCGCGCACGCGACCGC  
GAGGCGCGGCGTGACACCTCGCTGGAAGTTTGTCCGGGCGCGGAGCGCGGCGGAGCTTCGGGTTAGA  
GACCTAGCGCGCTGCAACCGCGCTAGCGCGCGCGAGCCTCCGTCGCGCGCGCGCGGGTTGGGGCTGCTGCTGTGC  
GCGGTTCTGGGGCGCGCTCGCCGGTCCGACAGCGCGGTCGCGGGGAACTTCGGGCAGCCCTCTGGGGTATGCCCGC  
GAGCGCCCATGCCCACTACTCTGCCGCTGCCCTGGGGACCTGCTGGACTCGATCGTAAGCGGCTAGCGCGCTCTT  
CCCGAGCCACTCGCTCCGCTCGGCTGCCGCTGGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCC  
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAATGAATTTGGAGACCATTCCTCAAATCTGGGACCA  
GTCTCGGCAAAATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATCTCGTGAACATTTGGGCCAACACA  
TTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTAGAGCTCCAAACTGCATTTTCAGCCCTACAG  
CTCAAAATCTGTATCTCAACAGCAACCGAGTCACTCAATGGAACCTGGGATTTTGAAATTTGGCCAAACACA  
CTCCTTGTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAAGATGTTTAAACTGCCCAACTGCAC  
CATCTCGAATTTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTTCCAAGGCTTGGTGCTCTGAAGTCT  
CTGAAATGCAAGAAATGGAGTAAAGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAATTTTG  
CAGCTGGACCATAAACAACCTAAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAATTCAT  
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCTCGGGAGTTCTGCCAAGACTCAGTGAGCTGGACCTTA  
ACTTTCAATCACTTATCAAGTTAGATGATTCAAGCTTCTTGGCCTTCCGGGGCTTTCAGTTTAAAGACTTTGGATCTGAAGAAC  
AACAACAGAGTCAGCTACATTTGCTGATTGGCTTCCGGGGCTTTCAGTTTAAAGACTTTGGATCTGAAGAAC  
AATGAATTTCTGGACTTGTGAAGACATGAATGAGTCTTCTCGGGCTTGACAACTGAGGCGAGTCAAGTAC  
CAAGGAATCGGATCGGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCAATTCGGAGCATCTAGACCTGAGT  
GACAAACGAATGCTCTTCAAGAGCAATGCAATTTTCAAAATGAGGACTGCAACATTTGCAATTAATACA  
TCAGCCCTTTTGTGCGATTTGCCAGCTTAAATGGCTCCCACTGGGCTGGCGGAAACAACCTTTCAGAGCTTTGTA  
AATGCGAGTTTTCAGCCATCTCAGCTGCTTAAAGGAAAGCAATTTTTCGCTTTAGCCAGATGGCTTGTGTGT  
GATGATTTTCCCAAACCCAGATCAGCTGCTCAGCCAGAAACACAGCTGGCAATAAAAGGTTTCCAATTTGAGTTTC  
ATCTGCTCAGCTGCGCAGCAGCATGATTTCCCAATGACTTTTTCCTTGGAAAAAGACAATGAACACTACTGTCATGAT  
GCTGAATGGAATAATTATGCACACCTTCGGGCGCAAAGTGGCGAGGTGATGGAGTATACCACCATCTCTCGGCTG  
CGCGAGGTGCAATTTTGCAGTGAAGGGAATATCAGTGTGTCATCTCCAATCACTTTGGTTCATCTACTCTGCTC  
AAAGCCAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCATGGATCTCACCATCCGAGCTCGGGCG  
ATGGCAGCTTGGAGTGTGCTGCTGTGGGSCACCAGCCTCCAGATAGCTGGCAGAGGATGGGGCGACAGAC  
TTCCAGCTGTCAGGGAGAGAGCATGATGTGATGCCGAGGATGACGTGTTCTTATGTGGATGTGAAGATA  
GAGGACATGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTAGCAAAATGCAACTCTGACTGTC  
CTAGAAACCACTATATTTTGGGCGCACTGTTGGACCGAAGTGAACCAAGGAGGAAACAGCCGCTCTACAGTGC  
ATTGCTGAGGAAGCCCTCCCCCTAACTGAATGAGCAGCAAGATGATAGCCATTGGTGGTAAACGAGAGGCAC  
TTTTTTCGAGCGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGATGTGCTGGGAAATACACATGTGAG  
ATGCTAACACCTTTGGCACTGAGAGGAGAAACGTCGCGCTCAGTGTGATGCCCATCTCAAACCTGCGACTCCCT  
CAGATGACAGCCCATCGTTAGAGATGACGGATGGGCCCATGTTGGGTGCTGATGATACATGAGCCGTGTTGCTGT  
GTGGTGGGCGACTCACTCGTGTGGGTGCTCATCATATACCACAAAGCGGAGGAATGAAGATTCAGCAGATTACC  
AACACAGATGACGATCTGCTCAGAAAGTGAAGCCACCAAGATTGTCACATCTTCAGGTGCTGATTTTCTTACCA  
CAACATGACAGTGTGGGACCTGCCATATTGACAAATAGCAGTGAAGCTGATGGGAAGCTGCCACAGATGCTGTC  
CTTTGTCGTTTGGGATCCACAGGCCCTATGATTTTGAAGGAAATGTGATGGCTCAGATCTTTTGAACA  
TATCATACAGGTGTCAGTCTGCCACAGAACAGTTTAAATGGACCACTAGTGGCCAGTATGACATAAGAAAG  
GAGTGTCACTCCATGTTCTCATCTTTCAGAAAGATCTGCGAAGCAGGAGTCTCAGTAATATATCTGCGCTTCACAT  
GTGAGGAAGCTACTTAACACTGATTACTCTCAAAATGAGGACTGGAATGGAATAATCTGTGCTTAACAGAGTCT  
TCTTTAGATTATTAGTGCAAATCCAGAGCCAGCGTCGGTTGCTCGAGTAATTTCTTTCAGGGTACCTTTGGAANA  
GCTCTCAGAGAGCTCCTCAGATAGCTTATTCAAGCTTTGGACAGCCATCAGATTGTCGCAAGAGGCTTTTAT  
TTGAAGCTCATCTTCCCAAGACTTTGGACTCTGGGTGAGAGGATGGGAAGAAAGAGCAGATTCTCAGGA  
GAAATCAATTTGATCTTTAACAGACTTTAGAAAACTACGAGACTTCTGCTTATGACTTGTGAC  
ACATAGACTGAATGAGACCAAGGAAAGCTTAACTACTACCTCAAGTGAACCTTTTAAAGAGAGAGAAAT  
CTTATGTTTTTATGAGGATTATGAATTTTAAAGGATAAAATGCTTTATTTATACAGATGAACCAAAATATAC  
AAAAAGTTATGAAATTTTTATCTGGAATGATGCTCATATAAGAAATACCTTTTAACTAATTTTTTAACTTTG  
TTTTATGTAAGAAATGATCTACTGATAATTAATGATTAATATGATTTATGTTTATTAATGCCAGA  
TTTCTTTTATGGAATAAGTACTAAAGCATTTTAAATAATACCTGCTTGTACCATTTTTTAAATGAGAGTT  
ACTTCATTATATTTTGCACATTATATTTAATAAAATGTCAATTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

09060325.071401

## FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDDSGGRGELQPPSGVAAERPCPTTCRLGLDLLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDDLSSNNISELQTAFPALQLKLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNISAIAPPKMKFLPQLQHLELNRRNIKNVDGLTFQGLGALKSLKMQR  
NGVTKLMDGAFWGLSNMEILQLDHNNTLITKGWLYGLLMLQELHLSQNAINRISPDWAEFC  
QKLESLDLTFNHLRLDDSSFLGLSLNTLHIGNNRVSYIADCAFRGLSSSLKTLDLKNNIEIS  
WTIEDMNGAFSGLDKLRRLILQGNRIRISITTKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQQLHLNTSSLLCDQLKWLQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDFF  
PKQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNEILLHDAEMENYAHLRAQGE  
VMEYTTILRLREVEFASGEKYQCVISNHFQSSYSVKAKLTVNMLPSPFTKTPMDLTIIRAGAMA  
RLECAAVGHPPAQIAWQDKGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRTVTVKGETAVLQCIAGGSPPPKLNWTKDSSPLVVTERHF  
FAAGNQLLIIVDSDDSDAGKYTCESMNTLGTGERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA  
TVGVVIAVVCVVGTSLVVVVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLDLRQ  
DGVVSSSGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCFPLGSTGPMY  
LKGNVYGSDDPFETYHTGCSPPDPRTVLMDHYEPSYIKKKECYPCHPSEESCERSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCNKSLLDFSANPEPASVSSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLDSSGEEDGKERTDFQENHICTFKQTLNRYTPNFQSYDLDT

### Signal sequence:

amino acids 1-27

### Transmembrane domain:

amino acids 808-828

### N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

### Glycosaminoglycan attachment site.

amino acids 886-890

### Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

### Tyrosine kinase phosphorylation site.

amino acids 667-675

### N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

### Leucine zipper pattern.

amino acids 58-80, 65-87

[illegible][illegible]

## **FIGURE 108**

MEGEEAEQPAWFHQPWRPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPREENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVDDCGGIDLREFPGDLP  
EHTNHLSQLNNQLEKIYPEELSRHLRLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK  
LTLAPRFLPNALISVDFAAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFGSSNV  
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF  
LEELNLSYNRITSQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHQLVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEEETR

### **Signal sequence:**

amino acids 1-48

### **N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

### **N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

### **Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557





## FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTGTCCTTTAGATTGTGA  
**AATG**TGGCTCAAGGCTTTCACAACCTTCTCTTTCTTTGCAACAGGTGCTTGCTCGGGGCTGA  
 AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTGAGGCCCTTACCTACCCGTC  
 CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA  
 CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTTGACTTGGAATACC  
 AACACAAGTTTCACCATGATGCCACCAATGTCATCTCTGCTTATCAACCCACTGCAGTTCCCT  
 GATGAAGGCAATTACATCGTGAAGGTCAACATTGAGGAAATGGAACCTTATCTGCCAGTCA  
 GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGAGATTATCCTCCCT  
 CTGGGGCTGTGGAGTATGTGGGGAACATGACCTGACATGCCATGTGGAAGGGGGCACTCGG  
 CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACAGCTCCACCTACTCCTTTTC  
 TCCCCAAAACAATACCCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
 GCCTGGTGAGGAACCTGTGCTGAGTGAATGGAAGTGATATCATTATGCCCATCATATATTAT  
 GGACCTTATGGACTTCAAGTGAATTCGTATAAAGGGCTAAAGTAGGGGAAGTGTCTTACTGT  
 TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
 CCTGGATTAGGAGGACTGACAATACATATATCATTAAGCATGGGCCCTCGCTTAGAAGTT  
 GCATCTGAGAAAGTAGCCAGAACAAATGGACTATGTGTGCTGTGCTTACAACAACATAAC  
 CGGCGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG  
 CACAGAAAGGAAAAATCATTTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTGATT  
 ATATCCATGTGTCTTCTCTTCCATGGAAAAAATATCAACCTTACAAAGTTATAAAAACAGAA  
 ACTAGAAGGCAGGCCAGAAACAGAAATACAGGAAGCTCAAACATTTTCAGGCCATGAAGATG  
 CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCAGATGTTTCTGGTGTTCACAG  
 ATTTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTGACAGTACAGT  
 GTATGAAGTTATTTCAGCATCCTCTGCCAGCAGCAAGACCATCCAGAGT**GA**ACTTTTCATGG  
 GCTAAACAGTACATTGAGTGAAATTTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAGT  
 ATATTAACTGGAATCAGTGAAAGAAACAGGACCAACACCTTACTCATTTATCCTTTTACA  
 TGCAGAATAGAGGCATTATGCAAAATGAACTGCAGGTTTTTCAGCATATACACAATGTCTT  
 GTGCAACAGAAAAACATGTTGGGAAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
 GGAGAACGAAAGTGACAGGGGTTTCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA  
 ATTAGTTCTACTCTACACTTTCACATATCATCAACACTGAGACTATCCTGTCTCACCTACAAA  
 TGTGGAACCTTTACATTGTTTCGATTTTTCAGCAGACTTGTGTTTTAAATTTTATTAGTG  
 TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTATTGTACAA  
 CAAAGTAATAAGGATGGTTGTGCACAAAAACAAACTATGCTTCTCTTTTTTTTCAATCACC  
 AGTAGTATTTTTTGAAGAAGCTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA  
 TTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCGTTTTTGCTTTTAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVGRQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNVKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGVEFTV  
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 341-359

### **N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

### **Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

### **Tyrosine kinase phosphorylation site.**

amino acids 272-280

### **N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18





## **FIGURE 114**

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFIKDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEQEAEDEEDVSE  
EEAESKEGTNKDFPQNAIQRSLGPSLATDKS

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 182-201

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

### **Tyrosine kinase phosphorylation site.**

amino acids 107-115

### **N-myristoylation site.**

amino acids 20-26, 192-198

### **Amidation site.**

amino acids 25-29

## FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG  
AAGGTCCTGGCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC  
ATTGCTGATGGCCTGGTTTGGTGTCTGTGAGCTGTGTGCAGGCCGAATTCTTACCTCTATTG  
GGCAGATGACTGACCTGATTTATGCAGAGAAAAGAGCTGGTGAGTCTCTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAAGCTTTCCAAGATTAAAGAGCTGGGCCAACAAAATGGAAGCCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCCGTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAAGACTCAGCTGCA  
GGTTTATGCGCAACCTCTCTGTGCGAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA  
GAGGGGAACCTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG  
GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTACAGGTGCTGGACTACCTCA  
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGCTCACCCGCCCGCTGCTC  
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAAATCTGCGGTACTTTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAACGTTAAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA  
TCTATGAGAGGCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGG  
GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA  
CAGGGCCCCACAGCTGCTCATTGCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA  
TCGTCAAGTACTACGATGTCTGTCTGATGAGGAAATCAGAGGATCAAGGAGATCGCAAAA  
CCTAAACTTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTTCACTGTGCGCAGCTA  
CCGGGTTTCCAAAAGCTCTTGGCTAGAGGAAGATGATGACCTGTTGTGGCCCGAGTAAATC  
GTCGGATGCAGCATATCAGGGTTAAACAGTAAAGACTGCAGAATTGTTACAGTTGCAAAAT  
TATGTAAGTGGGAGCAGTATGAACCGCACTTTCGACTTCTTAGGGACCTTTTGACAGCGG  
CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGTGTAGAAGCTG  
GTGGTGCCACCGTCTTCCCTGATCTGGGGCTGCAATTTGGCCTAAGAAAGGGTACAGCTGTG  
TTCTGTACAAACCTTTGCGAGCGGGGAAGGTGACTACCGAAACAGACATGCTGCCCTGCC  
TGTGCTGTGGGCTGCAAGTGGGTCTCCAAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCTTCCCTTCCCTGCTG  
CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCTTTGTATGTTCTTATCAGGCT  
GATTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCTCTGT  
GTGACTGAAGTCCAGCCCTTCCATTACAGCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA  
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCCTTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTTCAGTGAACCAAGTTCTGATACCTTGTTTACATGTTTGTGTTTTAT  
GGCATTTCTATCTATTGTGGCTTTTACAAAAAATAAAATGTCCTTACCAGAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAELVQSLKEYILVBEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAALKALMRLQDITYRLDPGTISRGEPLGTYQAMLSVDDCFGMGRSAYNEGDIYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQIGDLHRALELTRRLSLDPSHERAGGNLR  
YFEQLLEEREKTLTNQTEAELATPEGIYERPVLDYLPEDVYESLCRGEQVKTTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEEDWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDDPVVARVNRMRQHITGLTVKTABLLQVANYGVGGQYEPHFDFS  
RRPFDGSLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEQDYL  
TRHAACPVLVGCKWVSNKWPFHERGQEFLPCGSTEVD

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 115-119, 264-268

### **Glycosaminoglycan attachment site.**

amino acids 490-494

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

### **Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

### **Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

### **N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

### **Leucine zipper pattern.**

amino acids 213-235

## FIGURE 117

GCAGTATTGAGTTTIACTTCTCCTCTTTTATGTGGAAGACAGACCATAATCCCAGTGTGAGTGAAATGATTGT  
 TFCATTTATFACCGTTTGTGCTGGGGTGTAGTTCGACACCTTCACAGTTGAAGAGCAGGCAGAGGAGTTGTGA  
 AGACAGAGCAAACTCTTCTTGGGGATGCTGGTCTTGGAGCCAGCGGGCTTGTCTGTCTTTGGCTCATGTGACCC  
 CAGGTTCTGTGTTAAAACTGAAGGCTTACTACTGGCTGGTGGCCATCAATCCATTGATCTCTGAGGCTGTGCC  
 CCTGGGGCACCCACTTGGCAGGGCTTACACCACTGCGACTGAGCTCCCTGTTGGCTCTGCTCGGGCCAGCGCTTC  
 CCCTCATCTTAGGGCTGTCTCTGGGGTGCAGCTGAGCCTCCTGCGGGTTTCTTGGATCCAGGGGGAGGGAGAAG  
 ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTCCAGAGCTCGGCTAGACCAAGTG  
 ATGAAGACTTCAAACCCCGGATTGTCCCTACTACAGGGACCCCAAGGCCCTACAAGAAGGTGCTCAGGACTC  
 GGTCATCTCAGACAGAGCTGGGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTGACCTCCCGAGCTACACTGTCCA  
 CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCATCACTCCCTCGGTACTCTACTTCACTGGGCAGCGGGGG  
 CCGGGCTCCAGCAGGGATCAGGTTGGTGTCTATGGGATGAGCGGCCCGCTGGCTCATGTACAGAGCCCTGTC  
 GCCACTTCAACACACATTTGGGGCCGACTACGACTGGTCTTCTCATGTGAGGATGACACATATGTGACGGCCC  
 CCGCCTTGGCAGCCCTTGTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTCAATTG  
 GCGCAGGCAGCAGGCCCGGTACTGTCTATGGGGCTTTGGCTACCTGTTGTACGGAGTCTCCTGCTTCGCTCTGC  
 GGCCACATCTGGATGGCTGCCGAGGAGACATTTCACTGAGTCCCTCTGACGAGTGGCTTGGACGCTGCCTCATTTG  
 ACTCTCTGGGCGTGGCTGTGCTCAGACACACAGGGGCAGCAGTATCGCTCATTTGAACTGGCCAAAATAGGG  
 ACCCTGAGAAGGAAGSGAGCTCGGCTTTCTGAGTGCCTTCGCCGTGCAACCCTGTCTCCGAAGGTACCTCATGT  
 ACCGCTCCACAAACGCTTCAGCGCTTGGAGTTGGAGCGGGCTTACAGTGAATAGAACAACCTCGAGGCTCAGA  
 TCCGGAACCTGACCTGCTGACCCCGAAGGGGAGCGAGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCTCTTCA  
 CACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTACAGAGCAACACACTTCTCTGTCAGATGGGG  
 CTCACAGGTGCCACTACAGGGGGTAGCAGGGGCGACGTGGTGTGCTGAGACTGGGCTCGGCTGGAGCGCTCA  
 ATCGGGCTTACGCGCCGCTTGGCTTCCAGAAAGCAGCACTGCTCAACCGGCTTACCGGCTTCCAGCCAGCAC  
 GGGCATGGAGTACACCTGGACCTGTCTGTGGAATGTGTGACACAGCGTGGGACCCGGCGGGCCCTGGCTCGCA  
 GGGTCAGCTGTGCGGCCACTGAGCCGGGTGGAAATCCTACTATGCCCCATGTCTCATGAGGCCACCCGAGTGC  
 AGCTGGTGTGCCACTCCTGGTGGCTGAAGCTGCTCGAGCCCGGCTTTCTCGAGGCGTTTGGCAGCCAAATGTCC  
 TGGAGCCACAGAAATGCAATTGCTCACCCCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCCAG  
 ACCCATTTCTTGGGGTGAAGGCTGCGACAGCGGAGTTAGAGCGACGGTACCTGGGACGAGGCTGGCTGGCTCG  
 CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCTGTGGACACTCTCT  
 TCTTCCTTACCACGTTGTGGACAAGGCTGGGCCCGAAGTCTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT  
 GGCAGGCTTTCTTCCAGTCCATTTCCAGGAGTTCAATCCTGCCCTGTACCAACAGAGATCACCCCCAGGGCCCC  
 CGGGGGCTGGCCCTGACCCCCCTCCCTCCTGGTGTGACCCCTCCCGGGGGCTCCTATAGGGGGGAGATTG  
 ACCGGCAGGCTTCTGCGGAGGGCTGCTTCTACAACGTGACTACCTGGCGGCCGAGCCCGGCTGGCAGGTGAAC  
 TGGCAGGCCAGGAAGAGGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTCTCCGCTTCTCAGGGCTCC  
 ACCTCTTCTGGCCGTGAGAGCCAGGGCTGGTGCAAGATTCTCCCTGCGAGACTGAGGCCACCGCTCAGTGAAG  
 AACTCTACACCGCTGCGGCTCAGCAACTGGAGGGGCTAGGGGGCCGTGCCAGCTGGCTATGGCTCTCTTTG  
 AGCAGGAGAGGCCAATAGCACTTAGCCCGCTGGGGGCCCTAAACCTCATTAACCTTTCTTTGCTGCTCCCTCAGCC  
 CCAGGAAGGGCAGGCAAGATGTTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAATGTTATTAA  
 ACATGTCTCTGCG

05030303.07140

## **FIGURE 118**

MRLSSLLALLRPAFLIILGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPDSSRARLD  
QSDDEDKPRIVPYRYDPNPKPYKKVLRTYIQTGLGSRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLLYFTGQGRARAPAGMQVVSHGDERPAWLMSETLRHLHHTHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG  
DILSARPDENLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPHSRFEV  
LGWDVYFTEQHTFSCADGAPKCPLOGASRADVGDALETALEQLNRRYQPRLRFQKQRLNNGYR  
RFPDPARGMEYTLDDLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVPLLL  
VAEAAAAPAFLEAFAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKAAAAELERRYPG  
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFFP  
VHFQEFNPALSPQRSPPGPPGAGDPSPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLA  
RARLAGELAQEEEEALEGLEVMVDVFLRFSGLHLFRAVEPGLVQKFSRLDCSPRLSEELYHR  
CRLSNLEGLGGRAQLAMALFEQEQA NST

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 489-507

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250

## FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCTGTCCCCAAGCC  
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTGAAGGGTGTGATGCTTGG  
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTGAGTATACTGTATTATCCTTGTAAAACC  
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAACACTGTGACAAAAGCAG  
AGTTCCTTCAGTTCTGAAAAATGTTAAAGTGTTCGAGTCAATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACTG  
GTTCTTCTTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA  
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGCTTAAAGTGTAAGATCAATGAAAAGACTTAACAGCCTTCT  
CAATATCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAGGTAGTAGAAGGCTGTTGTTGAGATATGGCTGTACTTTTAAATGGACTGACTCCAA  
ATCAGATGCATGTGATGATGTATGGGGTATACGCCTTAGGGCATTGGGCATATTTTCAAT  
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTTGTATAGGACGTGTGTTGTGCTATTATTTGTAGTAGTAACACATATCCAA  
TACAGCTGTATGTTTCTTTTCTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTAAAAACATGAACATTGTAAATG  
TGTTGGAAGAAGTGTTTTAAAGATAATAATTTGCAAATAAACTATTAATAAATATTATAT  
GTGATAAATTCATAATATGAACATTAGAAATCTGTGGGGCACATATTTTGTGCTGATTGGTT  
AAAAAATTTTAAACAGGTCCTTTAGCGTCTTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAACCTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTATGTTCT  
AAGCCTCCCAAGTTCCAATGGATTGCGCTTCTCAAATGTACAACAAAGCACTAAAGAAA  
ATTAAAGTGAAAGTTGAAAAAT

CGCGGGGCTTCT





## FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG  
AAAAAGAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAGAAAAATGAATTTCATCTAAATCAT  
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAATGTTCTTATGGACTGTTGCT  
GGGATCCCCATCCTATTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT  
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT  
ACAATTATGGATCAGGTTCAAGCAAGTGTGTTGCCATTGAACTGGGAATATTTTCAATCC  
AGCTGCTACTTCTTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAACTGCTCAGC  
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA  
AACCTAAAATGAGAGAGTTTTTTATTGGACTGTCAGACCAGGTTGTCGAGGGTCAGTGGCAA  
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA  
CATAGCTACCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCCAAGGCAAAATTGGA  
ATGATGTAACTGTTTCCTCAATTATTTTCGGATTGTGAAATGGTAGGAATAAATCCTTTG  
AACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACCTCAAATGTGTAAGAAGGAAGAGCA  
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACCTCAAAGGACTTC  
ATAAGTATTGTGTTACTCTGATACAAATAAAAAATAAGTAGTTTTAAATGTTAAAAA  
AA  
AAAAA

## **FIGURE 122**

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALS LKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEFNNIATLEDCATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

### **Signal sequence:**

amino acids 1-42

### **N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

### **N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

# FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGTGGCCCCCTCAGCAACCCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTCGGCTCGGCTGCCCTGACTTCTTCTGCTGTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAATC  
TCAAAATCCAGCAATCGAACCCCGAGTGTGACAGGAATTTGAAAGGTGGAACTCTGTGCATCATACGGATTCCG  
AGACAAGTAGTACCCCGAGATCGAGTGGAGAAAATTCAGATGAACAAACACATATGTGTTTTTGACAAACAAA  
TTCAGGGAGACTTGGCGGCTCGTGACAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTAGGTGCTGTGCTCGAAATGACCGCAAGGAAATGATGAGATGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCAGAGGCTGTACCAAGATAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGATGAGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCATCGCCACGGATT  
CAGAGCCCAATCCAGATTTCGCAATTTCTTTCCACTTAACTCTGAAACAGGCACCTTTGGTGTTCACTGCTG  
TTCACAAAGGACGACTCTGGGAGTACTACTGTCATTGCTTCAATGACGACGCTCAGCCAGGCTGTGAGGAGCAG  
AGATGGAAGTCTATGACTGAACATTGGCGGAATTTAGGGGGGTTCTGGTTGCTCTTGTCTGATCTGCCCTCGA  
TCACGTTGGGCTCTGCTGTGCATACAGACCTGGCTACTTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCATGAGTGAAGTTAACTACATCCGACTGACGAGGAGGCGACTTCACACACAAGTCATCGTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCCGACGTCACATACCTTCTGCTAGAAAATCTCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTATTCAAGACTTTTGGTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGATTTTCTCAAGATGGACCCGGTAAATATAACACAAA  
GGAAGCGAAACTGGGTGCGTTCACTGAAGTTGGGTTTCTTAATCTGTTTCTGGCTGATTCGCGCATGATATTAGG  
GTGATCTTAAAGATTTGCTCAGCTAAACGCCCCGTCTGGGCCCTGTGTAGGCGAGCATGTTTACCACTGTGCTGT  
CAGCAGCCAGCACAGCCAGTCATGTAGATGAGGAGGTGGCTGACAGCACCAGCAGCGCATCCCGCGGGGAACCCA  
GAAAAGGCTTCTACACAGCAGCCTTACTTTCATCGGCCACAGACACCAGCCGAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCAATGTCATTTGAGTGTGAGAAGCTTTTGGATCAGCATTTTGTAAGAACAAACAAATCAGGAAG  
GTAAATTTGGTTGCTGGAAGAGGATCTTGGTGAGGAACCTGCTGTGTCCAACAGGGGTGACAGATTGAAGGAAA  
ACCTTCCTCTTAGGCTAAGTCTGAATGGTACTGAAATATGCTTTTCTATGGGTCTGTTTATTTTATAAAATTT  
TACATCTAAATTTTGGCTAAGGATGATTTTGGATTATGAAAAGAAAATTTCTATTAACTGTAATATATTGT  
CTACCAATGTAAATAACCTATTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTAAAT  
TGAAAAATTCAGTTTAAAGATTTTACCAAGGAATCTCTCATGGAAGTTTACTGTGATGTTCCTTTTCT  
CACACAAGTTTTAGCCTTTTTCACAGGGAACCTCATCTGTCTACACATCAGACCATAGTTGCTTAGGAAAACCTT  
TAAAAATTTCCAGTCTAAGCAATGTTGAAATCAGTTTGCATCTTCAAAAAGAACTCTCAGGTTAGCTTTGAACT  
GCCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG  
CCAGTCAGCTCTCGGGGTTGCGCCAGGGCGCCCCGCTCTAGCTCACTGTGTCCTGCTGTGCGCAGGAGGCCCT  
GCCATCCTTGGGCCCTGCGAGTGGCTGTGTCCCAGTGAGCTTTACTCAGTGGCCCTTGTCTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAAGGACATGCTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCTGTGAACAGACCTCT  
TTTTGGTTATGGATGGCTCAAAAAAGGGCCCCAATGCTATTTTTTTTTTAAAGTTTGTGTTAATTTATTTGTT  
AAGATTGTCTAAGGCGCAAAGCCAAATGCGAAATCAAGCTGTCAAGTACAATAACATTTTAAAAAGAAAATGGAT  
CCCCTGTTCCCTCTTGCCACAGAAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT  
GGAGTGGCGCCAGTCCAGCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCTGGCGGGGAGGAAAG  
TGAAACGCCCTGAATCAAAGCAGTTTTCTAATTTTGACTTTTAAATTTTTCATCGCGCGGAGACATGCTCCCATT  
TGTGGGGGAGCAATCCAGCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCTGGCGGGGAGGAAAG  
TGAAACGCCCTGAATCAAAGCAGTTTTCTAATTTTGACTTTTAAATTTTTCATCGCGCGGAGACATGCTCCCATT  
TGTGGGGGAGCAATCCAGCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCTGGCGGGGAGGAAAG  
GCGGTGCTGAGCTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCATCCACTGTGTGCTCGGA  
GAATGGCTCTCACTACTTGTCTTTTCACTTCCAGTGTCTTGGGTTTTTATCTTTGACAGCTTTTTTTT  
AATTGCATACAGAGACTGTGTGACTTTTTTTAGTTATGTGAAACACTTTGCGCGAGGCGGCTGGCCAGAGGCA  
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